

BRYOSTATIN SUBSTITUENTS

R_1 R_2

	a	b	b	e	d	c	d	d	c	c	c	b	c	c	c	c	c	
1	OH																	
2		OH																
4																		
5																		
6																		
7																		
8																		
9																		
10																		
11																		
12																		
13																		
14																		
15																		
16																		
17																		
18																		

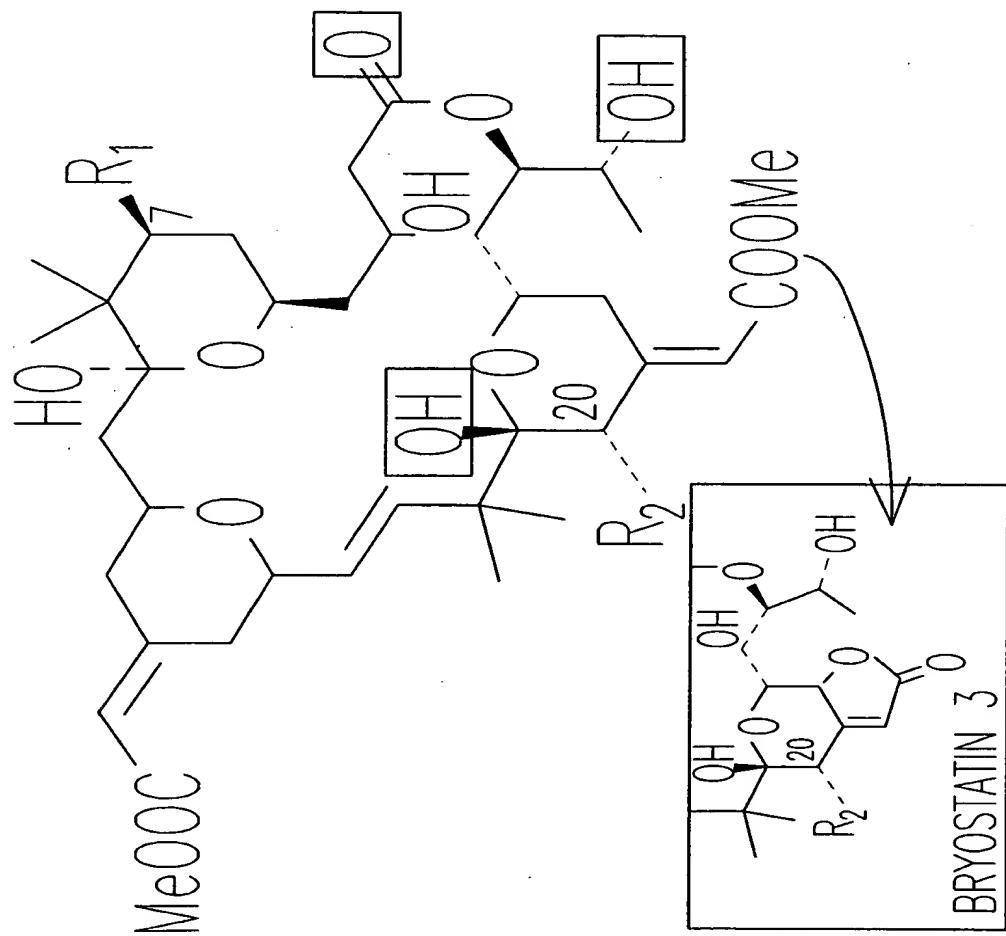


Fig. 1

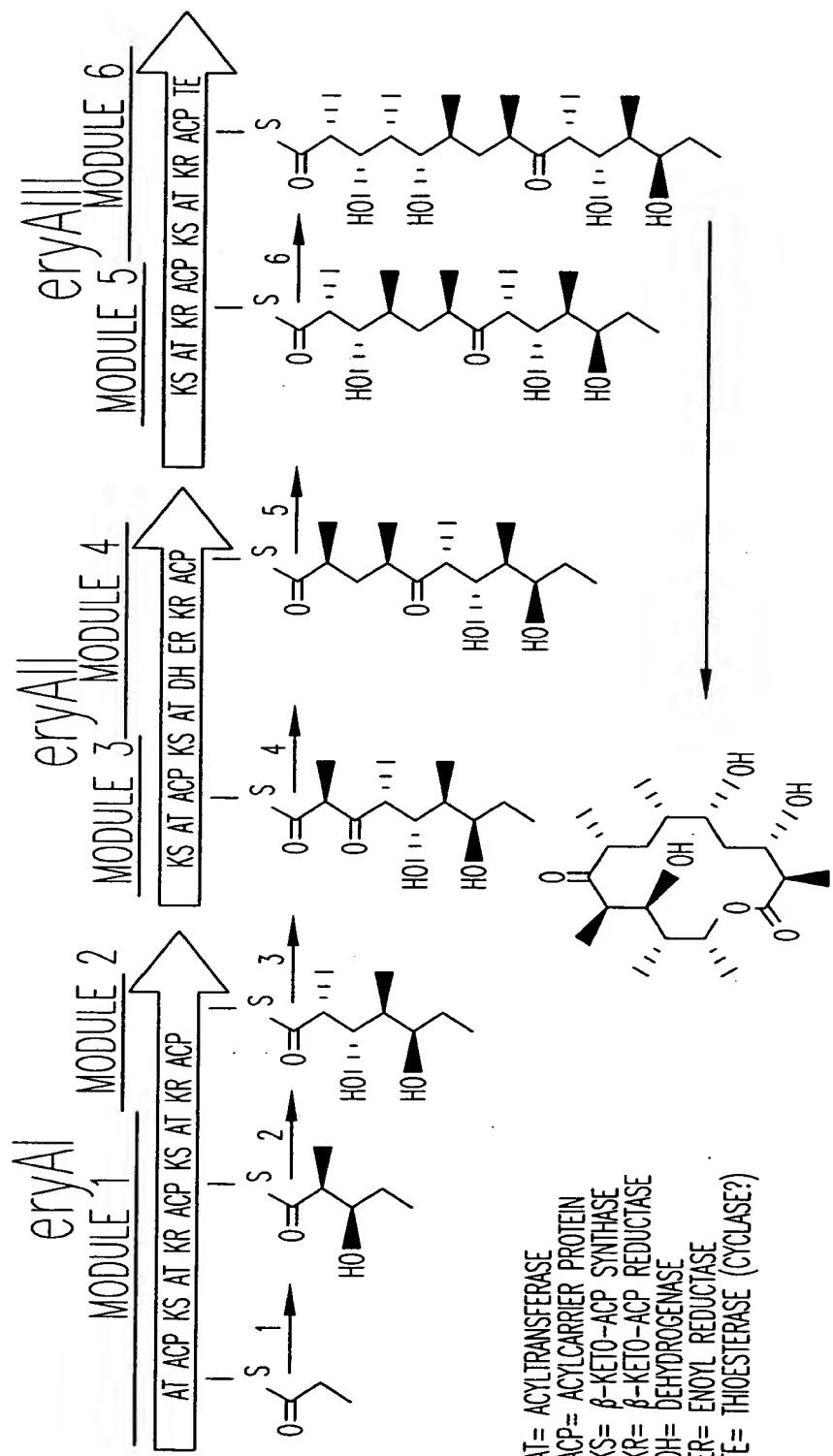


Fig. 2

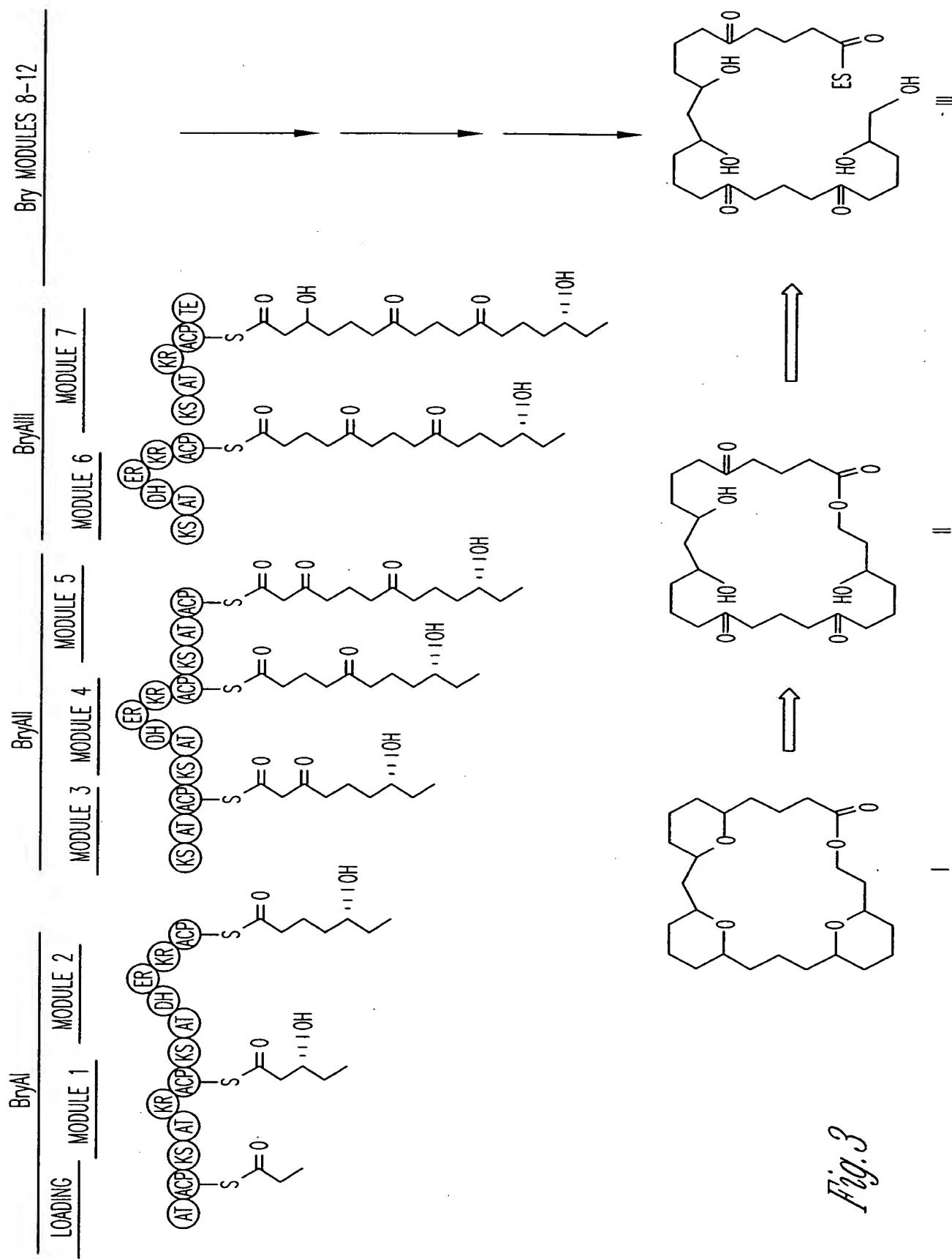


Fig. 3

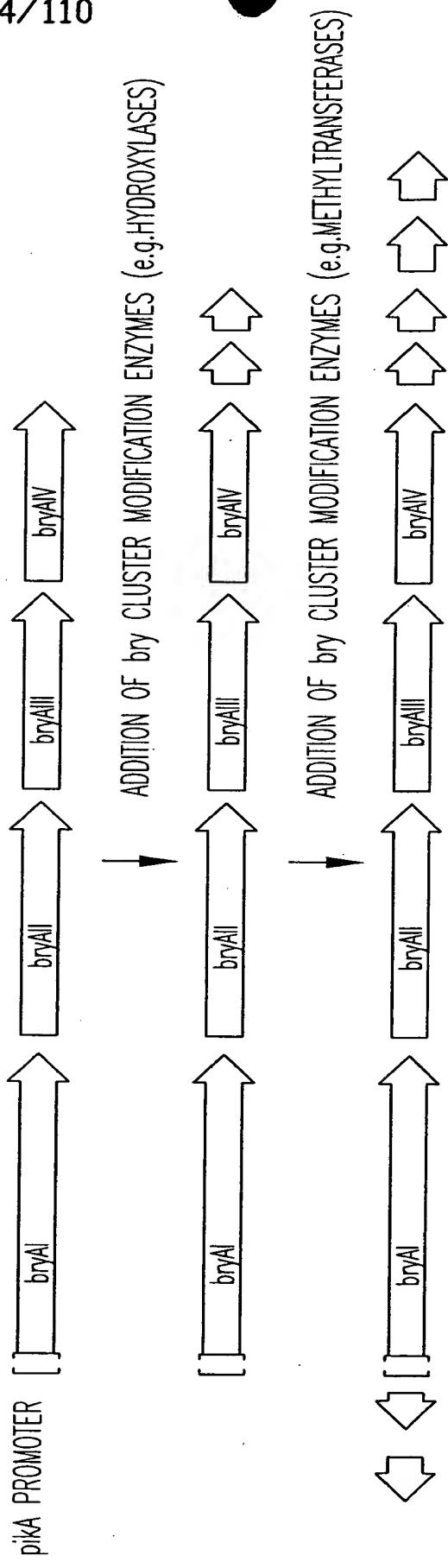
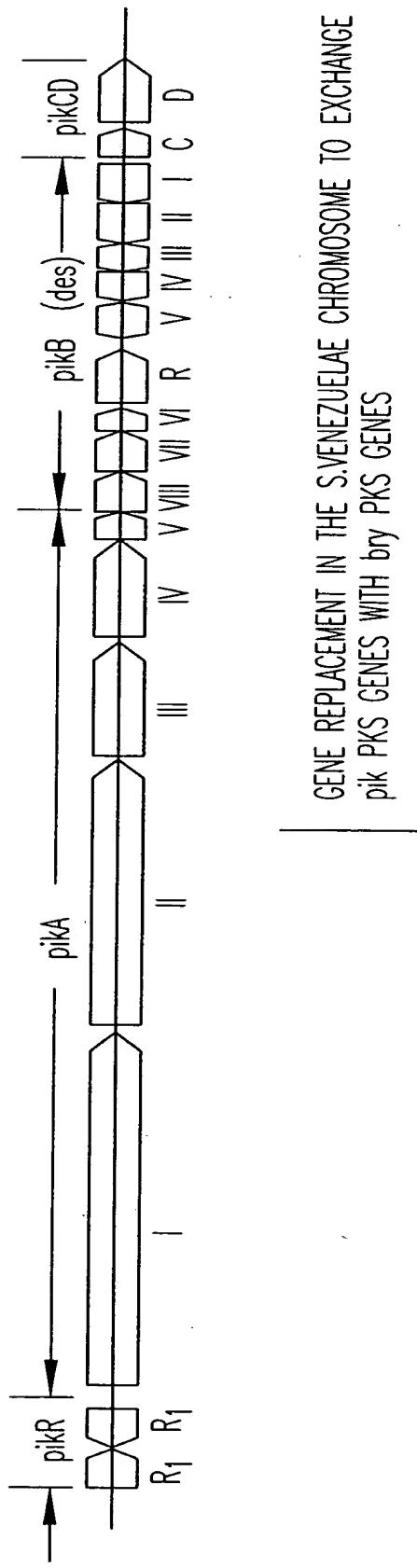


Fig. 4

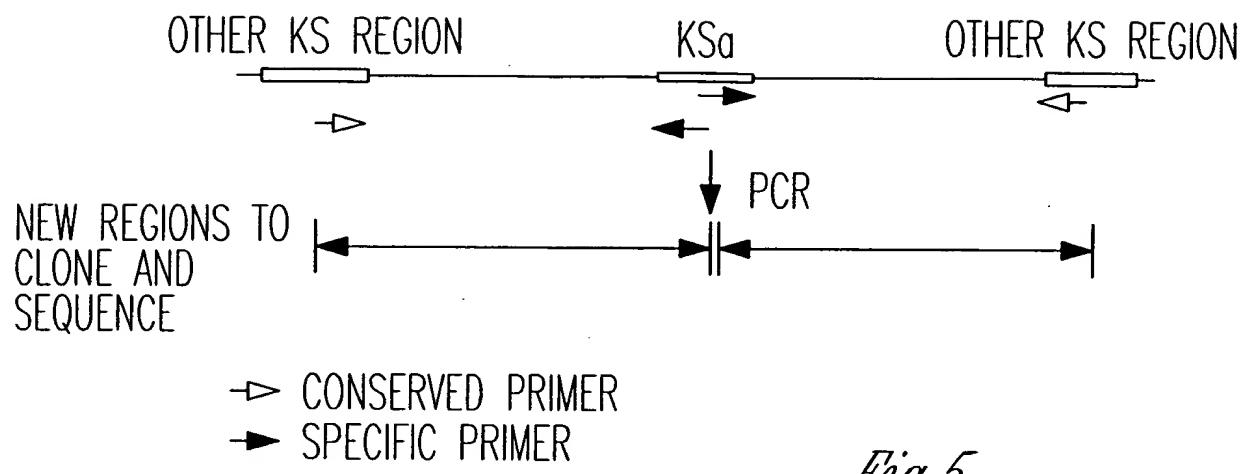


Fig. 5

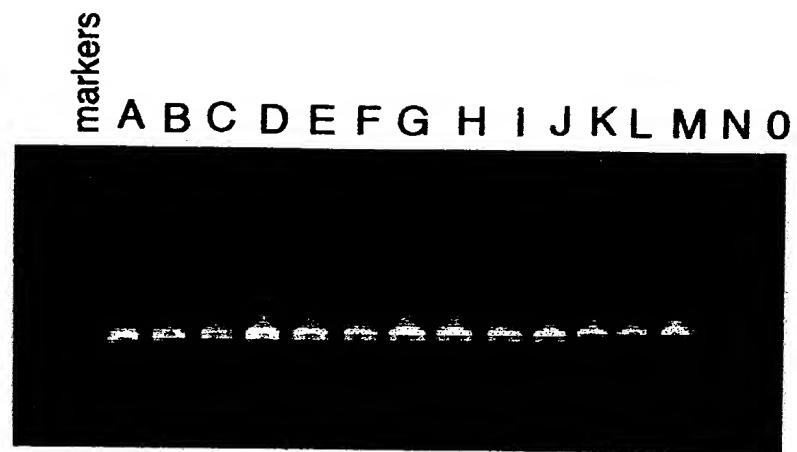


FIG. 6

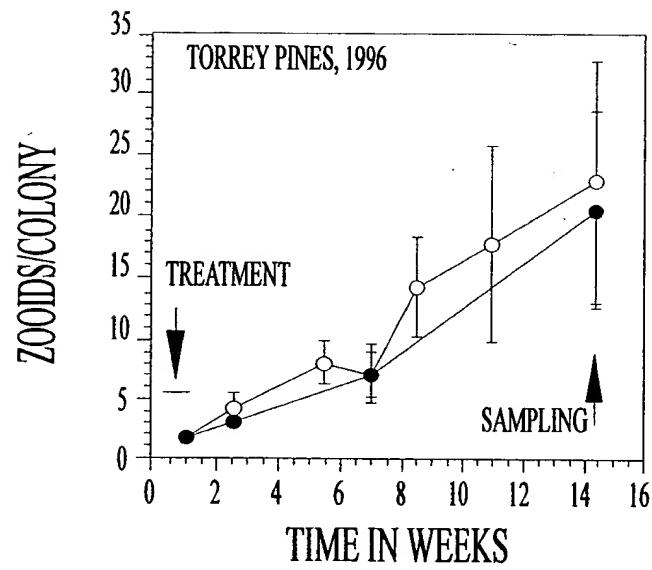


FIG. 7A

7/11/0

Control Treated



DGGE

Control Treated



KSa Amplification

FIG. 7B

FIG. 7C

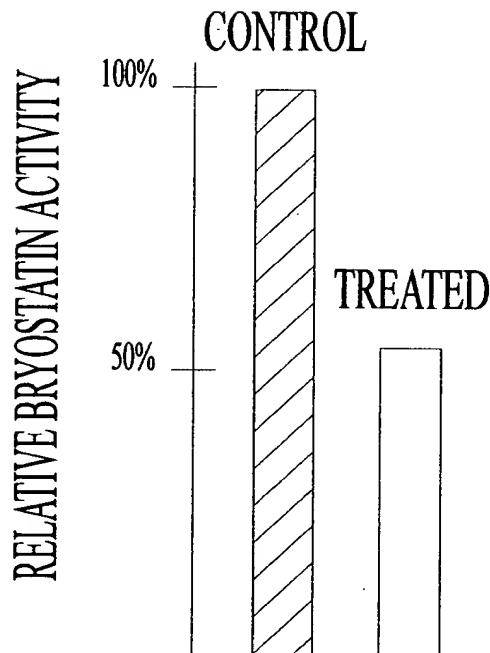


FIG. 7D

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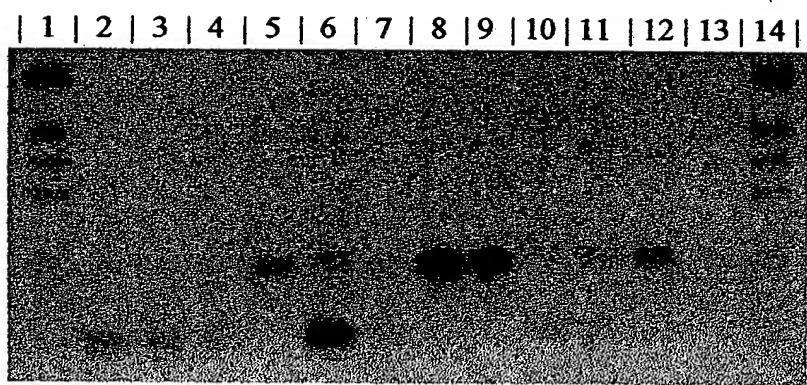


FIG. 8

00025938 " 03403

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TOP SECRET EYES ONLY

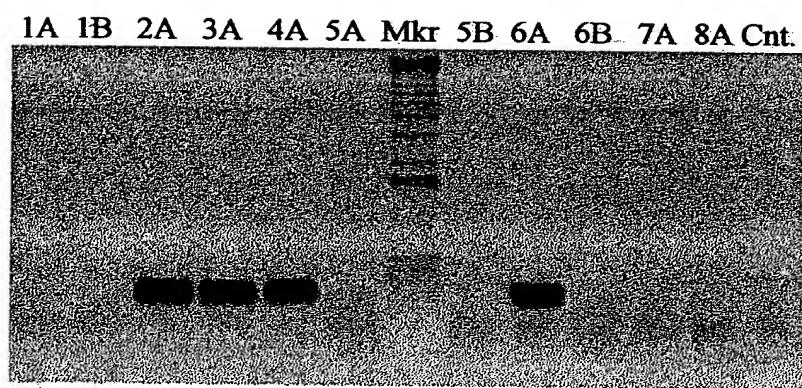


FIG. 9

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2A 3A Mkr. 4A 6A

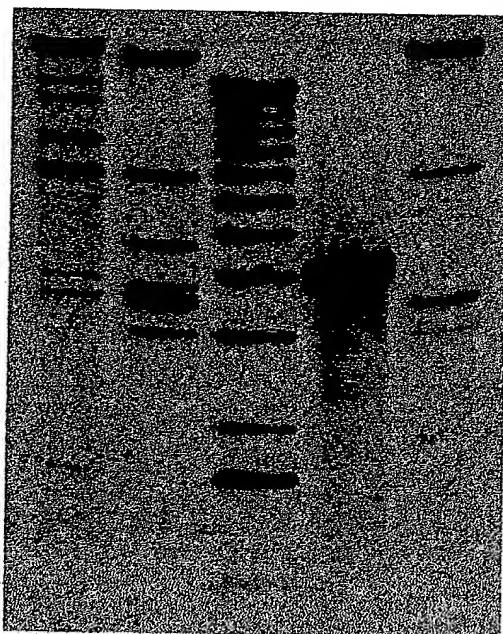


FIG. 10

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5A 5B 3A 6A

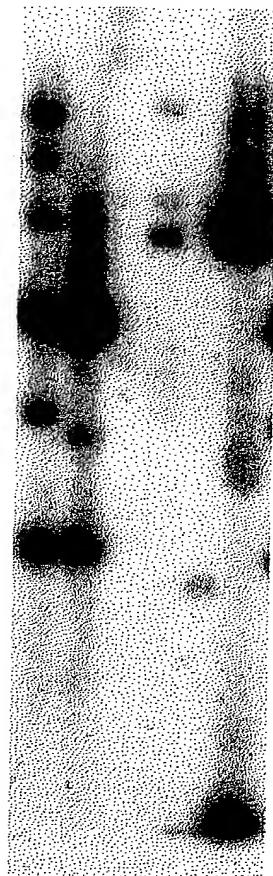


FIG. 11

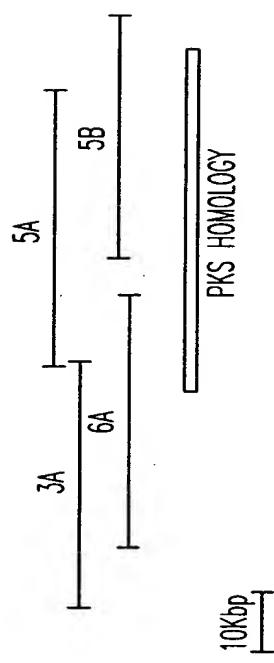


Fig. 12

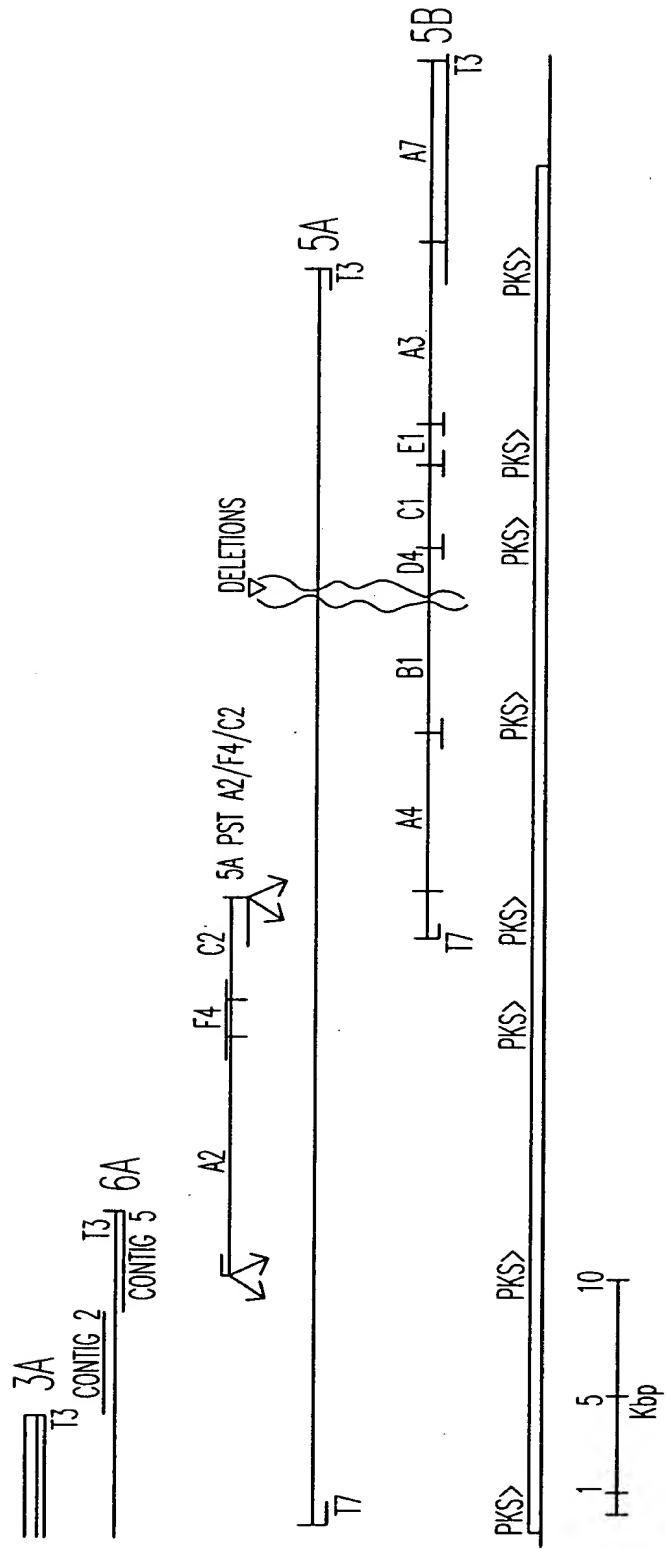


Fig. 13

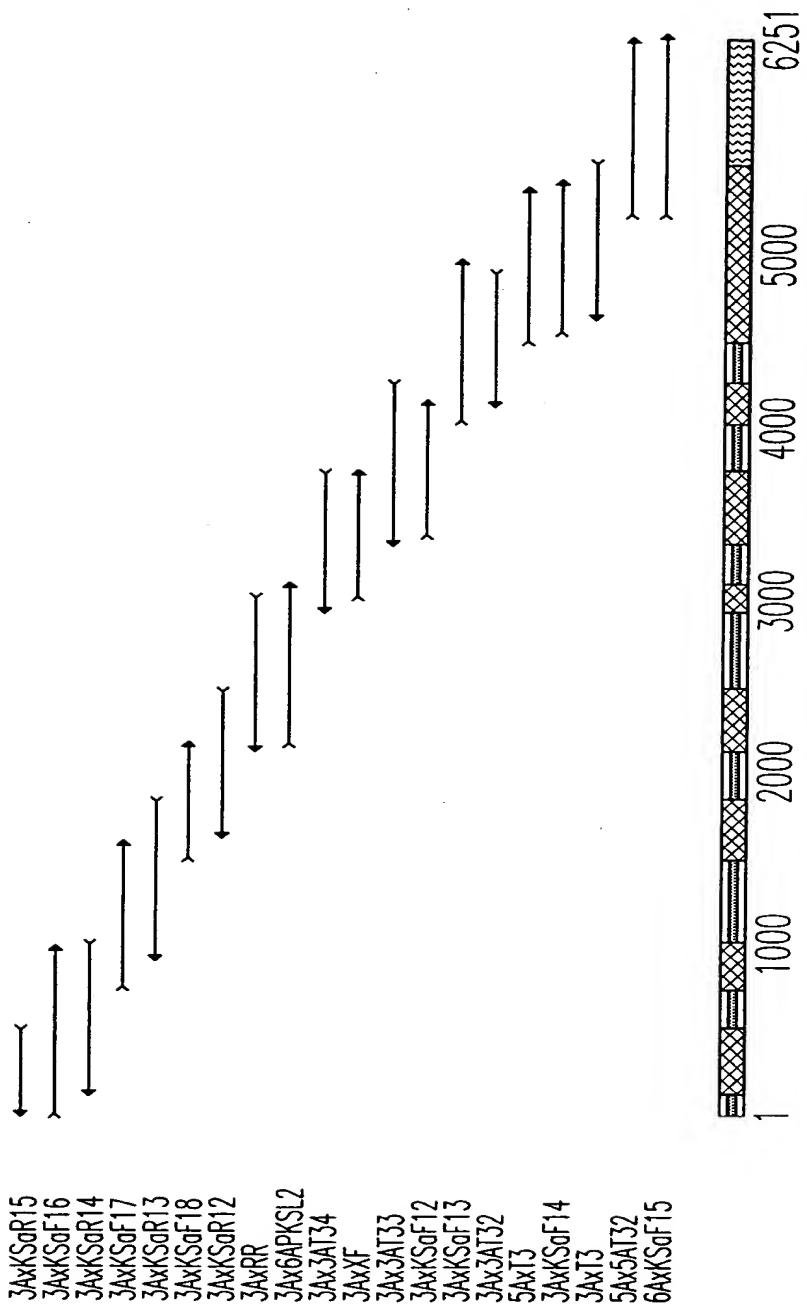


Fig. 14A

Nucleotide and Translated Amino Acid Sequence of PKS Cluster on Clone 3A

1 GAT GGA ACT CAT TAC CAC CCA CAA AAA AGT CCG TTT CTT CAA 42
43 CGC GGT TGA TTT AAT TAA CCA GCT AAT CAA CGA ACA ACA AAA 84
85 GCA GCA AAC GGG CAA ACT CAT CAG AGC CTT ATT GCA GGT GGA 126
127 TTG TTT AAG TAT TGA TGA ACT CGG TTA TAT CCC ATT CCC TAA 168
169 ATC CGG TGG GGC GTT GCT CTT CCA CCT CAT CAG TAA ACG GTA 210
211 TGA GAA GAC CAG TAT TAT CAT CAG CAC CAA TCT GGC TTT TGG 252
253 GGA ATG GAA CAG TGT GTT TGG TGA TGC CAA GAT GAC CAC CGC 294
295 GTT ATT GGA TCG TAT CAC GCA TCA TTG TTC AAT CAT CGA AAC 336
337 CAA GCA TGC GTC GTA TCG TTT TAA GCA GAG TCA GAA ACA GAC 378

379 ATG AAA GTA GCT TTC ACC GGT GGG ACA GTG TTA GAT GCA AAC 420
<<<TRANSPOASE ORF

421 CCC GGG TCA GCT TTA AGT GCA ATT TGA AAA CCA ATG TGA TAA 462
Possible transcription control sequences> -35 -10

463 TIG TGG CTA AGA TCA ATA AAA ATA AAA TTT TTT TAT TGA TTA 504
Inverted repeat> -----> -----<-----|

505 TGA TGA TCC ACG TTA AAA AAA ATA CTA TAA ATA TGA AAT AAT 546

547 ATT TCA ACT TTA TTT TTG ATG GTC GTT GTT GAG GAA TTT 588
PKS ORF START>>> M V V V E E F F
Possible SD sequence

589 GTG AGT TAT CGA GAT ATT TTG AAG GCT TTA CAG GAT GAA AAA 630
V S Y R D I L K A L Q D E K

631 ATT AGT TTT GAA GAG GCT AAA TAT AAG TTA ATA AAA AGA AAA 672
I S F E E A K Y K L I K R K

673 GAT AAA AAA TCA AAA CAG CGT TTA AAT CAT GAT CGT GAA TTA 714
D K K S K Q R L N H D R E L

715	AAT	CGA	TCG	ATG	AAT	ATT	ACG	CCA	AAA	ATA	GTG	AAT	AAT	TAC	756
	N	R	S	M	N	I	T	P	K	I	V	N	N	N	Y
757	GGT	TTA	GTA	TTA	TTG	GGC	GGT	CAT	TTA	TTT	GAA	GAA	CTC	CGT	798
	G	L	V	L	L	G	G	H	L	F	E	E	L	R	
799	CTG	AGT	GAA	TGG	AAA	GCT	GCC	AAC	CCT	AAC	CCT	AAT	GAA	GTT	840
	L	S	E	W	K	A	A	N	P	N	P	N	E	V	
841	AGC	ATT	CAG	GTC	AAG	GCA	TCC	GCC	ATT	AGT	TTT	ACC	GAT	ACC	882
	S	I	Q	V	K	A	S	A	I	S	F	T	D	T	
883	TTG	TGT	GTA	CAA	GGT	TTA	TAT	CCA	TCA	CAC	TAT	CCC	TTT	GTT	924
	L	C	V	Q	G	L	Y	P	S	H	Y	P	F	V	
925	CCG	GGC	TTT	GAA	GTA	TCG	GGA	GTG	ATT	CGT	CAA	GTG	GGT	GAA	966
	P	G	F	E	V	S	G	V	I	R	Q	V	G	E	
967	CAC	ATA	ACC	GAC	TTA	CAC	GTG	GGT	GAT	GAA	GTT	ATT	GGC	TTC	1008
	H	I	T	D	L	H	V	G	D	E	V	I	A	F	
1009	ACA	GGA	TCA	TCA	ATG	GGA	GGG	CAT	GCT	GCC	TAT	GTG	ACG	GTG	1050
	T	G	S	S	M	G	G	H	A	A	Y	V	T	V	
1051	CCA	CAA	GAT	TAC	GTG	GTA	CGA	AAA	CCC	AAG	GAC	TTA	TCT	TTT	1092
	P	Q	D	Y	V	V	R	K	P	K	D	L	S	F	

1093	GAG	GAT	GCC	TGT	AGC	TTC	CCA	TTG	GCT	TTT	GCG	ACC	GTC	TAT	1134
	E	D	A	C	S	F	P	L	A	F	A	T	V	Y	
1135	CAC	AGT	TTT	GCA	CGG	GGA	AAA	TTA	TCT	CAC	AAC	GAT	CAT	ATC	1176
	H	S	F	A	R	G	K	L	S	H	N	D	H	I	
1177	TTG	ATA	CAA	ACG	GCG	ACA	GGT	GGC	TGT	GGT	TTG	ATG	GCA	CTT	1218
	L	I	Q	T	A	T	G	G	C	G	L	M	A	L	
1219	CAG	TTG	GCG	CGT	TTA	AAG	CAG	TGT	GTG	TGT	TAT	GGG	ACC	TCC	1260
	Q	L	A	R	L	K	Q	C	V	C	Y	G	T	S	
1261	AGC	CGA	GAA	GAC	AAG	CTT	GCA	CTC	CTC	AAA	CAG	TGG	GCA	CTG	1302
	S	R	E	D	K	L	A	L	L	K	Q	W	A	L	
1303	CCC	TAC	GTC	TTC	AAT	TAT	AAG	ACG	TGC	AAT	ATT	GAT	GAG	GAG	1344
	P	Y	V	F	N	Y	K	T	C	N	I	D	E	E	
1345	ATT	CAA	CGC	GTC	AGT	GGT	CAT	CGA	GGT	GTC	GAT	GTC	GTC	TTA	1386
	I	Q	R	V	S	G	H	R	G	V	D	V	V	L	
1387	AAT	ATG	CTC	CCA	GGA	GAG	CAT	ATA	CAA	CAA	GGG	CTG	AAT	AGT	1428
	N	M	L	P	G	E	H	I	Q	Q	G	L	N	S	
1429	TTA	GCC	AAG	GGA	GGC	CGT	TAT	TTG	GAA	CTG	TCG	ATG	CAT	GGA	1470
	L	A	K	G	G	R	Y	L	E	L	S	M	H	G	

1471	TTG	TTA	ACG	AAC	GAA	CCT	GTC	AGT	CTG	TCT	CTG	CGT	CGT	TTT	1512
	L	L	T	N	E	P	V	S	L	S	S	L	R	F	
1513	AAT	CAA	TCC	GTT	CAA	ACC	ATC	AAT	TTA	CTG	GGG	TTA	CTC	AAT	1554
	N	Q	S	V	Q	T	I	N	L	L	G	L	L	N	
1555	AAG	GGT	GAT	GGC	TTT	ATC	GGG	TCT	GTA	TTA	GCG	CAA	ATG		1596
	K	G	D	G	F	I	F	S	V	L	A	Q	M		
1597	GTT	TCC	TGG	ATT	GAA	TCA	GGT	GAT	TTA	GTG	TCA	ACC	GTG	TCG	1638
	V	S	W	I	E	S	G	D	L	V	S	T	V	S	
1639	CGT	ATT	TAT	CCG	TTG	GAT	CAG	ATC	GGT	GAA	GCG	TTA	CGT	TTA	1680
	R	I	Y	P	L	D	Q	I	G	E	A	L	R	Y	
1681	GTC	TCT	GAA	GGG	GAG	CAT	ATA	GGT	AAA	GTC	GTT	GTG	AGT	CAT	1722
	V	S	E	G	E	H	I	G	K	V	V	V	S	H	
1723	ACA	GCG	ACA	GAG	CCG	ATG	GAT	TGC	AGA	CAG	CGC	TGT	ATT	GAC	1764
	T	A	T	E	P	M	D	C	R	Q	R	C	I	D	
1765	AAT	GTA	TTG	AAG	CAA	GGG	CAA	ATG	GCG	GCC	TTG	ACC	GCG	ACA	1806
	N	V	L	K	Q	G	Q	M	A	A	L	T	A	T	
1807	GGG	GGA	AAA	AGC	CGG	GTG	TGG	GGT	GGT	ACT	GTC	AAT	GAC	1848	
	G	G	K	S	R	V	W	G	G	T	G	V	N	D	

1849	AAA	CCG	TCT	CCT	GCT	GTT	GGT	ATA	GAG	GAG	CGT	TTA	TTG	GAA	1890
	K	P	S	P	A	V	G	I	E	E	R	L	L	E	
1891	GGG	ATA	GCG	GTC	ATT	GGT	CTG	TCA	GGC	CAG	TAT	CCG	AAG	TCG	1932
	G	I	A	V	I	G	L	S	G	Q	Y	P	K	S	
1933	AAG	ACA	CTG	GAG	CAA	TTT	TGG	CAG	ACC	CTA	GCG	GAT	GGA	GTG	1974
	K	T	L	E	Q	F	W	Q	T	L	A	D	G	V	
1975	GAT	TGC	ATC	TCA	GAG	ATT	CCT	GCT	GAT	CGC	TGG	TCG	TTA	GAA	2016
	D	C	I	S	E	I	P	A	D	R	W	S	L	E	
2017	GAG	TAT	TAC	TCG	CCA	ATA	CCG	GAA	GGG	GGT	AAA	ACG	TAT	TGT	2058
	E	Y	Y	S	P	I	P	E	G	G	K	T	Y	C	
2059	AAG	TGG	ATG	GGT	GTT	TG	GAG	GAC	ATG	GAT	TGT	TTT	GAT	CCG	2100
	K	W	M	G	V	L	E	D	M	D	C	F	D	P	
2101	TTG	TTT	TTT	GCG	ATA	TCT	CCT	CGG	GAA	GGG	GAA	GTG	ATG	GAC	2142
	L	F	F	A	I	S	P	R	E	A	E	V	M	D	
2143	CCA	CAG	CAA	CGG	TIA	TTT	TTA	GAG	AAT	GCA	TGG	AGT	TGT	ATA	2184
	P	Q	Q	R	L	F	L	E	N	A	W	S	C	I	
2185	GAG	GAT	GCG	GGG	ATT	AAC	CCT	AAG	ATG	TTA	TCC	CGT	AGT	CGA	2226
	E	D	A	G	I	N	P	K	M	L	S	R	S	R	

FIG 14B (cont'd)

2227	TGT	GGG	GTA	TTT	GGG	TGC	GGT	GCG	AAT	GAT	TAC	AGC	GCT	2268	
	C	G	V	F	V	G	C	G	A	N	D	Y	S	A	
2269	CTA	ATG	AAC	AGT	AGC	CAC	TCA	ACG	AGT	CTC	GAA	TTA	ATG	AAG	2310
	L	M	N	S	S	H	S	T	S	L	E	L	M	K	
2311	GAA	TTA	GGC	AAC	AAC	TCT	TCC	ATT	TTA	TCT	GCA	CGA	ATC	TCC	2352
	E	L	G	N	N	S	S	I	L	S	A	R	I	S	
2353	TAC	TTT	TTA	AAT	TTA	AAG	GGC	CCT	TGT	CTT	GGG	ATT	GAT	ACC	2394
	Y	F	L	N	L	K	G	P	C	L	A	I	D	T	
2395	GCA	TGT	TCT	TCT	TCA	TTA	GTG	GCC	ATT	GCC	GAG	TCG	TGT	AAT	2436
	A	C	S	S	S	L	V	A	I	A	E	S	C	N	
2437	AGT	CTG	GTG	TTG	GGT	ACT	AGT	GAC	TTG	GCG	TTG	GCA	GGT	GGA	2478
	S	L	V	L	G	T	S	D	L	A	L	A	G	G	
2479	GTG	TTG	CTG	ATG	CCA	GGT	CCA	TCC	TTA	CAT	ATA	GGT	TTG	AGT	2520
	V	L	L	M	P	G	P	S	L	H	I	G	L	S	
2521	CAT	GGA	GAA	ATG	TTA	TCA	GTA	GAT	GGT	CGC	TGC	TTT	ACC	TTT	2562
	H	G	E	M	L	S	V	D	G	R	C	F	T	F	
2563	GAC	CAA	CGG	GCC	AAC	GGT	TTT	GTA	CCT	GGA	GAG	GGT	GTC	GGC	2604
	D	Q	R	A	N	G	F	V	P	G	E	G	V	G	

2605 GTT GTC TTG TTA AAA CGC ATG TCG GAT GCG GTG CGT GAT GGT 2646
 V V L L K R M S D A V R D G
 2647 GAT CCC ATT CGT GCA GTG ATA CGG GGC TGG GGT GTG AAT CAG 2688
 D P I R A V I R G W G V N Q

2689 GAT GGT AGA AGT AAT GGT ATT ACG GCG CCG AGT TCA AAA GCG 2730
 D G R S N G I T A P S S K A

2731 CAA AGT GCT CTG GAG CAA GAG GTT TAT CAA CGT TTT AAT ATT 2772
 Q S A L E Q E V Y Q R F N I

2773 GAT CCA TCG AGC ATT ACC TTA GTC GAA GCA CAC GGA ACG GGC 2814
 D P S S I T L V E A H G T G
 2815 ACC AAA TTG GGT GAT CCG ATA GAA GTC GAG GCA TTG GCA GAA 2856
 T K L G D P I E V E A L A E

2857 TCG TTT CGA GTC TAT ACG GAC AAG CGT CAT TAC TGT GCT CTG 2898
 S F R V Y T D K R H Y C A L

2899 GGG TCG GTA AAA AGT ATT GGT CAT TTG GGG GTA GGT GCT 2940
 G S V K S N I G H L G V G A

2941 GGG ATA GCG GGC GTG ACC AAA GTA TTG TTA TCT TTG CAG CAT 2982
 G I A G V T K V L L S L Q H

2983	CGC	ATG	TTA	CCA	CCG	ACG	ATT	CAT	TGT	GAG	GAT	GTA	AAC	CCA	3024
	R	M	L	P	P	T	I	H	C	E	D	V	N	P	
3025	CAG	ATT	GCG	TTG	GAA	GGT	AGC	CCC	TTT	TAT	ATC	AAT	ACG	GAA	3066
	Q	I	A	L	E	G	S	P	F	Y	I	N	T	E	
3067	TTA	AAG	CCT	TGG	CAG	TCT	GGT	GAC	AGT	ATA	CCA	CGA	CGG	GCT	3108
	L	K	P	W	Q	S	G	D	S	I	P	R	R	A	
3109	GGT	GTC	AGT	TCT	TTT	GGA	TTC	AGT	GGT	ACC	AAT	GCA	CAT	CTT	3150
	G	V	S	S	F	G	F	S	G	T	N	A	H	L	
3151	GTA	TTG	GAG	GAA	TAT	CTT	CCT	CAC	TCG	ACA	GGA	ACA	ATA	GAG	3192
	V	L	E	E	Y	L	P	H	S	T	G	T	I	E	
3193	TCG	TTT	GCT	GCG	AAT	CAT	GCA	AGT	ACA	GT	ATT	CCT	TTG	3234	
	S	F	A	A	N	H	A	S	T	V	I	I	P	L	
3235	TCA	GCG	AAA	AGT	CAT	AAT	AGT	TTA	TAC	ACA	TAT	GCT	CAA	ACG	3276
	S	A	K	S	H	N	S	L	Y	T	Y	A	Q	T	
3277	CTA	TTG	ATA	TTT	TTA	AAA	CGT	AGT	CAG	GT	ACT	GAC	GCT	AAA	3318
	L	L	I	F	L	K	R	S	Q	V	T	D	A	K	
3319	AAA	ATC	ACA	ATA	GAT	CAC	ATG	GAA	TGT	CGC	TTG	GAT	TTA	3360	
	K	I	T	I	D	H	M	E	C	R	L	L	D	L	

3361	GCC	TAT	ACT	TTG	CAA	GTG	GGT	CGC	GAG	GCA	ATG	GAC	AAA	CGG	3402
	A	Y	T	L	Q	V	G	R	E	A	M	D	K	R	
3403	ATA	AGT	TTT	ATT	GTC	AAC	ACA	AAG	CAA	GCA	CTC	GTG	GAA	AAG	3444
	I	S	F	I	V	N	T	K	Q	A	L	V	E	K	
3445	CTA	AAT	GCT	TTT	CTA	GAG	AAG	AAG	ACT	ATA	ACA	GAC	TGT	3486	
	L	N	A	F	L	E	K	E	K	T	I	T	D	C	
3487	TAC	CAC	TAT	TTA	TTT	GAT	AGT	GAC	AAA	CCG	TCT	ACA	GAA	ATT	3528
	Y	H	Y	L	F	D	S	D	K	P	S	T	E	I	
3529	TTC	CGT	TTA	GAC	GAA	GAT	GAC	AAA	GTA	TTA	ATA	AAC	AGC	TGG	3570
	F	R	L	D	E	D	D	K	V	L	I	N	S	W	
3571	ATA	AGT	CAA	AGT	CAA	TAT	CAC	AAA	TTA	GCC	GAA	GCC	TGG	AGC	3612
	I	S	Q	S	Q	Y	H	K	L	A	E	A	W	S	
3613	CAA	GGA	CTC	GAT	ATC	GAC	TGG	ACG	CTA	CTC	TAT	ACC	CAC	TCA	3654
	Q	G	L	D	I	D	W	T	L	L	Y	T	H	S	
3655	TCA	ACC	CCT	CGT	CGC	ATT	AGC	CTG	CCC	ACG	TAT	CCC	TTT	GCC	3696
	S	T	P	R	R	I	S	L	P	T	Y	P	F	A	
3697	AGA	GAC	CGC	TAC	TGG	CTA	CCA	GAA	AAA	CCA	CGC	TAT	AAC	GCG	3738
	R	D	R	Y	W	L	P	E	K	P	R	Y	N	A	

3739	GCT	AAT	CAT	CCG	GTA	TCC	AAC	CAT	CAA	ACA	ACC	ACT	CAG	AAT	3780
	A	N	H	P	V	S	N	H	Q	T	T	T	Q	N	
3781	CAC	TCA	CGC	TTT	GCC	ATT	GAT	ACG	GAT	CAC	GAT	GTC	GTT	GCC	3822
	H	S	R	F	A	I	D	T	D	H	D	V	V	A	
3823	GAG	ATC	ATG	CAA	AAG	ACA	CAT	CAA	CAG	GAA	CTG	GAA	CAA	TGG	3864
	E	I	M	Q	K	T	H	Q	Q	E	L	E	Q	W	
3865	TTA	TTA	AAA	CTG	TG	TTG	GTG	CAA	TTG	CAA	CAT	ATG	GGA	TTA	3906
	L	L	K	L	F	V	Q	L	Q	H	M	G	L		
3907	TTT	CAA	CAT	CGT	GTC	TTT	GAG	ACA	GCG	ACC	GCT	CTA	CGT	CAA	3948
	F	Q	H	R	V	F	E	T	A	T	A	L	R	Q	
3949	AGT	GCA	GGC	ATC	GTT	GAT	AAA	TAT	GAT	CGC	TGG	TGG	CAT	GAG	3990
	S	A	G	I	V	D	K	Y	D	R	W	W	H	E	
3991	TGT	TTA	AGC	GTT	TTA	CAG	GAT	GCG	GGT	TAT	CTT	GAA	TGG	AAA	4032
	C	L	S	V	L	Q	D	A	G	Y	L	E	W	K	
4033	GAC	GAT	AGC	GTA	GGC	GGC	GCA	CAG	GCA	TTG	GAG	TCT	GAA	TCG	4074
	D	D	S	V	A	A	A	Q	A	L	E	S	E	S	
4075	CAA	GAG	GCA	TGG	TGG	AGC	CGA	TGG	AAC	ACG	GAG	TAT	AAG	CAT	4116
	Q	E	A	W	W	S	R	W	N	T	E	Y	K	H	

4117	TAC	CAG	AAT	GAT	CCG	GAA	AAA	AAG	ACG	TTA	GCG	ATA	TTG	ATT	4158
	Y	Q	N	D	P	E	K	K	T	L	A	I	L	I	
4159	AAC	GAT	TGC	TTA	CAG	GCA	TTA	CCA	GGG	GTG	TTA	AGT	GGT	GAG	4200
	N	D	C	L	Q	A	L	P	G	V	L	S	G	E	
4201	CAA	TTA	ATA	ACGG	GAT	ATT	ATT	TTC	CCC	AAT	GGT	TCG	ATG	GAG	4242
	Q	L	I	T	D	I	I	F	P	N	G	S	M	E	
4243	AAA	ATG	GAA	GGC	TTA	TAT	AAA	AAT	AAT	AGG	ATT	GCA	GAT	TAT	4284
	K	M	E	G	L	Y	K	N	N	R	I	A	D	Y	
4285	TGT	AAT	CAG	TGT	GTT	GGA	GAC	CTG	CTC	GTC	CAG	TTT	ATT	GAA	4326
	C	N	Q	C	V	G	D	L	L	V	Q	F	I	E	
4327	GCA	CGT	CTG	TCA	AGA	GAT	GCC	AAT	GCG	AGG	ATA	CGG	ATT	ATC	4368
	A	R	L	S	R	D	A	N	A	R	I	R	I	I	
4369	GAA	ATT	GGG	GCC	GGT	ACG	GGG	GGC	ACC	ACC	GCG	ATA	GTG	CTG	4410
	E	I	G	A	G	T	G	G	T	T	A	I	V	L	
4411	CCA	ATG	TTA	CAA	GCC	TAT	CAG	GAT	CAT	ATC	GAT	ACG	TAT	TGT	4452
	P	M	L	Q	A	Y	Q	D	H	I	D	T	Y	C	
4453	TAT	ACG	GAT	GTT	TCC	AAA	GCC	TTT	TTG	ATG	CAT	GGA	CAG	GAA	4494
	Y	T	D	V	S	K	A	F	L	M	H	G	Q	E	

4495	CAC TAC GGC GAA CAA TAC CCC TAT CTG AGT TAT TGC CTC TGT TGT 4536	H Y G E Q Y P Y L S Y C L C
4537	AAT ATT GAA CAG GAC TTA GTG GCT CAA GGA ATC AGC GTT GGT 4578	N I E Q D L V A Q G I S V G
4579	GAT TAT GAT ATT GCG ATC GCA GCC AAT GTA TTA CAT GCC ACG 4620	D Y D I A I A N V L H A T
4621	CGG AAT ATA CAC GAA ACG GTC AGC CAT GTG AGG CAG GCA TTG 4662	R N I H E T V S H V R Q A L
4663	GCG GCC AAC GGT TTA TTG ATT TTA AAT GAG TTT AGC CAA AAA 4704	A A N G L I L N E F S Q K
4705	AGC GTT TTT TCG AGT GTG ATA TTT GGT TTG ATC GAT GGT TGG 4746	S V F S S V I F G L I D G W
4747	GCC TTA TCT GAA GAT ACG GGA TTG CGT ATT CCT GGA AGC CCA 4788	A L S E D T G L R I P G S P
4789	GGG TTA TAT CCT AAG CAG TGG CAA GCG GTA CTG GAG GCG TCG 4830	G L Y P K Q W Q A V L E A S
4831	GGT TTT GGT GAC GTG GAA TTT CCG CTC CAT GAC GCT CGT GAG 4872	G F G D V E F P L H D A R E

4873	TTG	GGT	CAA	CAA	ATC	ATC	CTG	GCA	ACC	AAC	GCC	CAT	GCG	AAC	4914
	L	G	Q	Q	I	I	L	A	T	N	A	H	A	N	
4915	GTT	GCT	AGC	GAT	CTT	GCG	ACA	TCG	GTG	ATT	GAT	CAT	GCC	CCC	4956
	V	A	S	D	L	A	T	S	V	I	D	H	A	P	
4957	AAG	AGA	TTG	CCA	TCC	GCC	GAG	GTC	AGC	ATG	GAT	GAG	AGA	GTG	4998
	K	R	L	P	S	A	E	V	S	M	D	E	R	V	
4999	AGC	CAT	GAT	GCC	ATG	ATG	AAG	GCA	TCG	GTC	AAA	CAG	TTG	TTG	5040
	S	H	D	A	M	M	K	A	S	V	K	Q	L	L	
5041	GTA	GAG	CAA	TTA	TCC	CAG	TCT	TTA	AAA	CTG	GAT	ATG	AAT	GAG	5082
	V	E	Q	L	S	Q	S	L	K	L	D	M	N	E	
5083	ATT	CAC	CCT	GAC	GAA	TCC	TTT	GCC	GAT	TAT	GGT	GTT	GAT	TCC	5124
	I	H	P	D	E	S	F	A	D	Y	G	V	L	S	
5125	ATT	ACC	GGT	GCT	AGT	TTT	ATT	CAA	CAG	CTT	AAT	GAC	ACG	CTG	5166
	I	T	G	A	S	F	I	Q	Q	L	N	D	T	L	
5167	ACA	CTG	ACT	TTA	AAG	ACG	GTG	TGT	TTG	TTT	GAT	CAC	AGC	TCG	5208
	T	L	T	L	K	T	V	C	L	F	D	H	S	S	
5209	GTA	AAC	CGA	CTG	ACG	GCC	TAT	CTG	TTA	TCT	GAC	TAT	GGT	GAT	5250
	V	N	R	L	T	A	Y	L	L	S	D	Y	G	D	

5251	GAT	ATC	GCG	CAG	TGG	TTA	GCA	ACG	GCA	CCA	GCG	TTG	GTT	GAT	5292
	D	I	A	Q	W	L	A	T	A	P	A	L	V	D	
5293	CAT	CCA	CAG	AGT	GTC	GTC	AGT	CAG	GTC	TTG	CCT	GAA	AGG	TCG	5334
	H	P	Q	S	V	V	S	Q	V	L	P	E	R	S	
5335	CCA	GCA	AGC	ACA	CAA	GCC	AAG	CCC	TTG	CCT	TCA	GTC	CCC	CCT	5376
	P	A	S	T	Q	A	K	P	L	P	S	V	P	P	
5377	TCG	TTA	TCG	ATG	GAG	TCA	CCC	GTT	CAA	CAG	GAG	TCG	ATA	GCG	5418
	S	L	S	M	E	S	P	V	Q	Q	E	S	I	A	
5419	ATT	ATT	GGT	ATG	AGC	GGA	CGG	TTT	GCG	GCG	TCA	GAA	AAC	CTG	5460
	I	I	G	M	S	G	R	F	A	A	S	E	N	L	
5461	GAA	GGG	TTT	TGG	CAA	CAG	TTG	GCA	CAG	GGT	GTG	GAT	TTG	GTC	5502
	E	A	F	W	Q	Q	L	A	Q	G	V	D	L	V	
5503	GAA	CCC	GCG	TCA	CGT	TGG	GGG	CCA	CAA	GCG	GAG	ACT	TAC	TAC	5544
	E	P	A	S	R	W	G	P	Q	A	E	T	Y	Y	
5545	GGC	AGT	TTT	CTC	AAG	GAT	ATG	GAT	CAA	TTT	GAT	CCT	CTC	TTT	5586
	G	S	F	L	K	D	M	D	Q	F	D	P	L	F	
5587	TTT	AAT	CTC	TCC	GGT	GTG	GAA	GCG	AGT	TAT	ATG	GAC	CCG	CAA	5628
	F	N	L	S	G	V	E	A	S	Y	M	D	P	Q	

FIG 14B (cont'd)

5629	CAA	CGT	TGT	TTT	CTG	GAG	GAA	TCC	TGG	AAT	GCA	CTG	GAG	AAT	5670
	Q	R	C	F	L	E	E	S	W	N	A	L	E	N	
5671	GCG	GGT	TAT	GTG	GGT	GAT	GGC	ATA	GAA	GGC	AAG	CGT	TGT	GGT	5712
	A	G	Y	V	G	D	G	I	E	G	K	R	C	G	
5713	ATT	TAT	GCC	GGT	TGC	GTG	TCC	GGT	GAC	TAC	GCA	CAA	CTG	TTG	5754
	I	Y	A	G	C	V	S	G	D	Y	A	Q	L	L	
5755	GGC	GAC	CAA	CCC	CCG	CCG	CAG	GCT	TTT	TGG	GGC	AAT	GCC	AGT	5796
	G	D	Q	P	P	P	Q	A	F	W	G	N	A	S	
5797	TCT	ATT	ATT	CCC	GCC	CGG	ATT	GCC	TAT	TAT	TTA	AAT	CTT	CAG	5838
	S	I	I	P	A	R	I	A	Y	Y	L	N	L	Q	
5839	GGC	CCT	GCT	ACC	GCG	GTG	GAT	ACT	GCC	TGC	TCA	AGT	TCT	CTG	5880
	G	P	A	T	A	V	D	T	A	C	S	S	S	L	
5881	GTG	GCG	GTG	CAT	TTG	GCC	TGC	CAG	GCC	CTA	CAC	CTG	GAT	GAA	5922
	V	A	V	H	L	A	C	Q	A	L	H	L	D	E	
5923	ATG	GAG	ATG	GCC	TTG	GCA	GGA	GGT	GTG	TCT	CTT	TAT	CCA	ACC	5964
	M	E	M	A	L	A	G	G	V	S	L	Y	P	T	
5965	CCC	ATC	ATT	GTA	TGA	GTC	TTT	GCG	TGG	TGC	AGA	TAT			6000
	P	I	I	V	Z	V	F	A	W	C	R	Y			

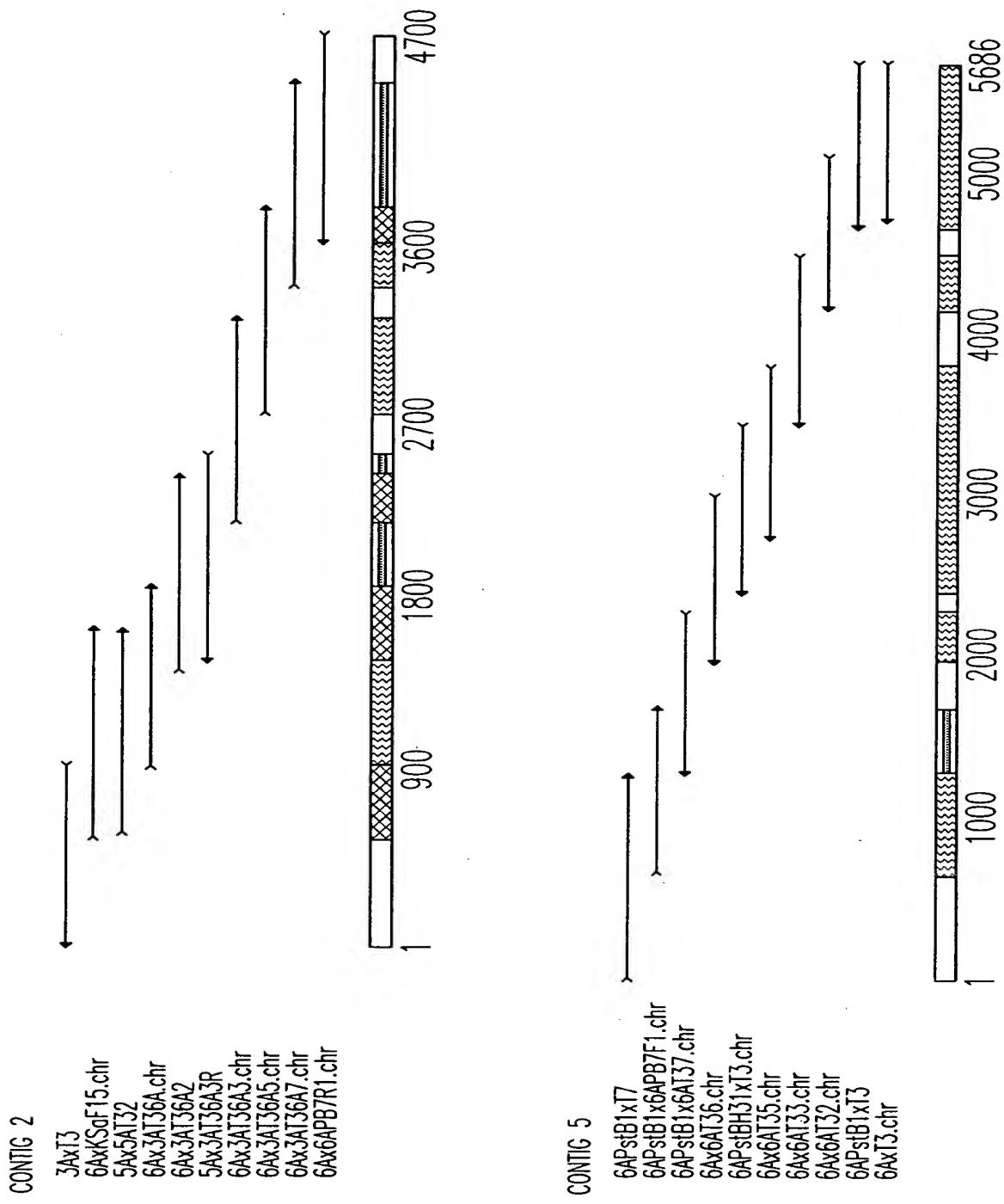


Fig. 15A

*Contig Sequences from Cosmid 6A**Contig 2*

ANCAATTATNACATCCNCGGAAAANACGAACGGTCACCATNTAGGCAG
 GCATTGCGGCCAACGGTTATTTTTAAATGAGTTAACCAAAAAAGNGTT
 TTTGNAGTGTAAATTGGTTGNGANGGTTGGCCTTATTTAANANAGGGA
 TTGNGTATTCTTGAAACCCAGGGTTATTCCTAACAGTGCACCGTACT
 GAGGCCTCGGNTTGGTTACGTGAATTCCGCTCCATGACGCTCGTAGT
 TGGGTCAACAAATCATCCTGGCAACCAACGCCATGCGAACGTTTAGCG
 ATCTTGCACATCGGTGATTGATCATGCCCAAGAGATTGCCATCCGCC
 GAGGTCAGCATGGATAAAGAGTAGCCATGATGCCATGATGAAGGCATCGG
 TCAAACAGTTGTTAGAGCAATTATCCCAGTCTTAAACTGGATATG
 AATGAGATTCACCCGTACGAATCCTTGCCGATTATGGTGGATTCCAT
 TACCGGTGCTAGTTATTCAACAGCTTAATGACACGCTGACACTGAYTT
 KRAAGACKKTGTGTTGCTTGATCACAGCTCGTAAACCGACTGACGGCC
 TATCTGTTATCTGACTATGGTGATGATATCGCGAGTGGTAGCAACGGC
 ACCAGCGTTGGTTGATCATCCACAGAGTGTGTCAGTCAGGTGTTGCCTG
 AAAGGTGCCAGCAAGCACACAAGCCAAGCCCTGCCTCAGTCCCCCT
 TCGTTATCGATGGAGTCACCCGTTAACAGGAGTCGATAGCGATTATTGG
 TATGAGCGGACGGTTGCGCGTCAGAAAACCTGGAAGCGTTGGCAAC
 AGTTGGCACAGGGTGTGGATTGGTCGAACCCGCGTCACGTTGGGGCCA
 CAAGCGGAGACTTACTACGGCAGKTYCTCAAGGATATGGATCAATTGA
 TCCTCTCTTTAATCTCTCCGGTGTGGAAGCGAGTTATATGGACCCGC
 ACAACGTTGTTCTGGAGGAATCCTGGAATGCACTGGAGAATGCGGGT
 TATGTGGGTGATGGCATAGAAGGCAAGCGTTGTTGATTTATGCCGGTTG
 CGTGTCCGGTGAACCGACAACGTTGGCGACCAACCCGCCAGG
 CTTTTGGGCAATGCCAGTTCTATTATTCCGCCGGATTGCCTATTAT
 TTAAATCTTCAGGGCCCTGCTACCGCGGTGGATACTGCCGCTCAAGTTC
 TCTGGTGGCGGTGCATTGGCCTGCCAGGCCCTACACCTGGATGAAATGG
 AGATGGCCTGGCAGGAGGTGTCTCTTATCCAACCC : ATCATTGTA
 TGAGTCTTGCCTGGTGAGATATGCTCTCTCGAGGGGGCGTTGCCACA
 : GCTTGATGCCTGTGCCACGGTATCGTATTKGTAATGGTGGGGK
 GGTG : GG : GCTAAAACGCTTGTCCGGCATTGGCCGGATGGC : AATCA
 TATTCAAGGAGTGATTGCTGGCAGTGGTATCAA : TCAAAACGGTCTAGT
 AAMTGGGAATACGGCACCCAGTGCACAAATSCAAAGAACGCTGGWAAC
 GTTGGGTT : TATGATCGCTTGTGDTGYYAACCTTKAGCAHATKAGCATGKT
 CGAAGGCCVDTGGACAGGGCACGRDYTTAGGTGKACCCCGTTGAAYRT
 DAAACYTTAMACCCGGVGTTAGACACTWADACGSAATAAGAAHAATD
 HTGVGCHATCGSGTCGGC : CAAAACCAATATGGAMACYGGSACCATGGT
 WGGCTGGGTDTGGGGGGCTTGTGGATRTKKAAG : TGGTGGTGTGCGAT
 GCAACACCGGAAACACCTCCATCGCTACATTACTCAGGGCAATCCG

FIG. 15B

P07570-2009272000

AATATTGACTTGATCGCAGTCCTTTATGTGAACACCGAGCTCGTGA
 TTGGTCGGTGGGTGAAGGAGAGACCGTTGTGCGACGGTAGCGCCTTG
 GATTAGTGGTACCAATGCCATGCAGTGATAGAAGAACGCCAGTC
 GTGCCAACATGAAGAGCAGCCGGTTATTAAGTGGTCTATCGCGC
 ATAGTGATGATCAATTACGGCAGCAAGGTTGAGAACTTATCGGGTTAT
 TGTGAGCATCACCTGAGTTGGATGTGGCAARTCYTGAGRTTATACCTT
 ATTG : TTGGG : TCGTCAACATTGG : TCGCATCGTCTGGCTGGT : TGGCG
 T : GTGATCTTGAGGATTGCGGCGGTACTGGATCAGTGG : TTGGTCAG
 GGTAAGGCTCCCCGAGTGTATGT : GTCT : GCA : TTGGCTGAGGGTGAACC
 AC : GTCTA : CAAGTTCTCTACAGCACGTTGTAATGAATGTATAAGAGC
 A : TGCAGTGAGTCCTGTTCTGCGAATCACTATGTGGACGCCGTATCGACG
 GTGGGGAWTTATATGTCAGGGTTATCCATTGGAGTATGGTGTGTTGTT
 TGSCCAKGGCWATRRWCKTWTSSKTTKCCGAMCTAKSSGTTSCWARKC
 AGCGTTGTTGGTACCAACAAACAATAAGCCACTCCACAGTGGATGCTATA
 TCACAGCATGCTTTTACATCCTTGTACATCGAAATACTTCGGACTT
 TTCATGTCAGCAGTTAGCTCCACATTAATGGAGTGAATTTTCTTA
 CTGACCACCTTATTCTAGGCAAAAGATAATTGCCCGAGCCGMYMTTTC
 GAAATGGTCCGAGAGGCCATCAAACAAGCTGTGGATTGGATAATT
 TGAAGTTGTTATTCAAGCTCAATGATATTGTATGGACAAAGTGAATTG
 TTGATGATGATATCAAAGAAGTACATATTGATCTTTGTAGAAAATGG
 CAGTGAATCATGCTTAACGCATGAGTTGATAGGCAAAACATATCGCTTA
 ACTATGAAGTTATACGAAAATAGTGAGGGAAATGGCAGGCAGAATAAA
 AAAATTATTATAATCACSGCATGGCACCTTGAGTTCTTGAATAACAA
 CCGGAGGTTGTAGATCTTGATGAACTACSCMGCCMCTATAAATCAASCAA
 GTCTTANATGCTGAACAAATGTTATTGGCGTTGGAAATCAATARGTGT
 CAKWWTGGTACAGGCMCCGATGTATARATACTSGTWTATWTGGT
 TCAAGTATTARCMAAACTYYTWTGCCAGAAATTGCAGGAGAWTTGGATA
 ARTSCTTGTGACACAGGTTACAGCTTGAATGATATCATGTTAGCC
 CGATTATATCTTGACCCCCAAGTCGACGCTCCCTTGCTCTKGWMAAAS
 TKKAAWTWAYSGAAAAYGTCAGATTCTATGTGGGTTGGATTCKAAAT
 TCTTATCGACAGACASAAGTCTCCACGCTCAGCCGTTAATGATATA
 AACATCTGACATTGATCTTGGACGCTCAAGGAAAAGTATGTGTGCGA
 ATGCGAGGTTCTGTCTGGGTTTGCCAAACAAATGGTTAATTCACTA
 SCAGAAGAACGTTACAGCTTGAATAACCAGCAAGCACC : TTACTTT
 TCCAATCCCAGGTATGGCGTT : CGCCAGACTCTTATCCAAGTGGCAATT
 AACCCCTACCTTAAWTGATGCCGGTCCATCCTGGGGTGGTTGACGNAT
 TTGAAATATGGACTTAATGTAGAAAATAGAAGGATGTAGAGGTTATTGA
 CCTTACACTCCAAACCACTGGATTACAGGATCGCTACTTGTGATATT
 TGCAC TGAGGTATTGAAATTGAAAANGACGTAATGATAGATAAATCC
 GTACAACCAGTACTGATTCAAGTTAGTTCTAATGATGGAGAACAGG
 GGTATTCAACCAGTTATTGGCATTACTAAAGGTGGCTCGCTCAGAAAACC

FIG 15B (cont'd)

CCAAAGTGATTACACAATTCAAGTACAATAGTCCCGCAAACCTCGC
 AAAATTACTACGGATTATCACTGAAAATAGTCATGATATAACACATGCA
 GAAATTCTGTTATCACTGGNATCAACGTGAATGTTGKTTGGKAASCAG
 TACCCAAATCTACAAAAACYTTACTCAACTCCCTGGAAATCTAACAGWGT
 TTATYTCWTTMCGGGAGGKACCGGTGGAATTAGCGTCACAGTTGTCAAA
 GCGWTAGCAGTGAGTCCCACAAAATCGGTATTAATCTKGTAGGKCSKTC
 ACCACTCMATGRTGAAAAGAAATCTTAWTAACTAGAACCTGGRATCCGTT
 GGGGGACCATTATTAAWTMCTATCARAACRGATGTAAGCCAACANGGATC
 AAGTTAAAGCWTGTTAAARAAATTKTTCASCAWTMCGGTCAATTGAAW
 GGKGKTTTSYATTGTGCAGGTATTGTCAACGACAATTTATTCTCAAAAAA
 GTCCTCGACAGAATACAAAGAGGTATTGTGTNTAAAGTATCNGGTNCTG
 TCAATTAGACCAGGCANACANAGNATAGAGATGGATTTCTATNNNTA
 NTAAAAACGTTATCTGCAGTATTGGANNACAGNACAGGGTNTTAGATA
 ATNGTCCAAATACTTTCCAGGTGTTGGTAAANGGATTGGAANCCAA

Contig 5

GCNCTTNCCCGGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTG
 CAGTATTGGAAATGCAGGTCAATCAGATTATTCAACGGCAAATAAATT
 ATGGATGAGTTGCACGCTATCGTAATGCTCTGGTCAATCGCAAAGAGCG
 CTATGGTTAACACTATCGATTAATTGGCCGTACTGGAGAGAAGGAGGTA
 TGAGTATTGAGGAAAATTGAAAATATAATGCAAGAGAATACCGGTATG
 TCCGCCCTGGAGACATCACAAGGTATTGAAGTATTACAAAGAGCTGGCA
 GTTGCAGTACACGCAATTGTTGGTAATGGTCGGAGAGATGAAGCGAATGG
 AGAGCTTTTGACAAGCAGGGTTCGAGCAGATTCTGTGGTATCGCC
 GATACTGTCAGCGAGAATAAAACCTCGACTATTGAGAATCTTCAGCCGA
 TGTAGATACATTACCAATTGAGGTTCAAGCATAACATATGGAACAAA
 AAACCCCTGATTACTTAAAAATGTATTGCCACACACAAATCCCC
 GAGAAAAATATTATGTCATGAAACATTGGATAAAACGGAGTTGATT
 ATTGTTGGTGATGAAAATGACCAATCAATTGGAAAAGTATTGGAAAAT
 TATCTAAAACCTATTGAAATATCAAACCAATTGCGAATGGCGAT
 TATTGCGAATTTCATGATGAAAAGTTAAGGGAGTTTCAGATAGA
 TAGCAAACATCTATGTTAAATAATCACGGAGAGATTGAAGTTCAAAAAA
 AAGGGGATGAACCATCGGTTGGAGACAGATATAACTCAGCTGGATGCCGT
 GCCTATCTCGGTTATATCGCCTGTCAGCAGTGAATCATCAACCAAAA
 AAATGTTAACATGGTCCMATANTCATCAGCCAGTAATGGGATATTGGC
 GAWTATTGGGTCTGAGKGGTCGTTATTCCMCAAGCCTGAGAAATATNGG
 AGGAAATACTGGGAAGAAATTGTTGTCAGGCAAGGGACTGGTATTAN
 CNGGAAANTCCAAANGGAGCCGTTGGGATTGGSAAAGACTATTWYACMS
 MTNNNGATCCSTATTCAAGCCMGGTGGACATCGCAGTAAATNGGGKGGT
 TTTATTGCGGATGTTGATAAGTTGATCCGTTATTGTTAATATTCCCC
 TAGKGRGGKGGAGCTYRCTSATCCTCAGGAAYKWTATTTYCTAGRGTCC

FIG 15B (cont'd)

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GCGTKGGCTGCATTGGAAGACCCTGGAWATTGCCGGGNATTATTCGAAA
 TGTTGTCAAGGACTAAATCTTCATTCTCGTCGGRAGATGTTGGTGT
 TATGTGGRAGTRATGTCTTCAGAATATCAGTTGTTGCTTGAACAGAA
 WTTACGTGGTCACCCATATCCTCNGGTTGGAGTTATGCCAGTATTGCT
 AMCCSGGTGTCTTATGTTTARATCTACACNGGCCAASCATGACAGTGG
 ATMCGATGTGKTCTARTTCGTTAACGACGCTWCACCTAGCATGKCAGGGA
 TTTAAAACGGGKCGAAACTGACCYGGGTATTGKCGGKGGAGTTAAWATT
 ACCATTCACCCMATAAAATATYAGGCSTGAGTCACGCYCAAATTATTY
 TACTAGTGGTSGTGCAAARTTTGGTGAACAGGGACAGGGTTATATCC
 CTGGTGAAGGAGTGGGTGCCATAATACTGAAGCGCTGGTCATGCCGAG
 CGTGACGGTGATCATATTATGGTGTAAAGGCAGTGCCGTTAACCA
 TGGTGGTAAAACCAACGGCTATAACGTTCTAACCGAATGCACAAACAGC
 AAGTGGTGAGTCGTGCACTACGAGAACGCCAGTAAACCCCCATCATGTG
 ACTTATATTGAGGCACATGGAACAGGAACCCAATTGGTGACCCGATAGA
 AATTACTGKTCTRAMMAAGCGTTCAATAGTTGACCAATGAGCTTGGTT
 TAAGCGCTGTGSCAAACMATYKGKTTGATCGGTCARKGAAGTCAAA
 TATAGGCATTGTGAGYCASCAGCCGGTGTGCAGCTATTGAAAGTA
 TTGTTACAAATGCAACACGGTCAAATAGTCCCTTCTTACATTCAAAAG
 CATTGAATCCAATATTGATTTACTGTGACTCCCTTGTAGTAAACCAA
 GGGTTATTGGACTGAAACGACTTGAAGTTGAAGGAAAGAGGGTRCCGAG
 AATKGCTKKYMWYWCKYTTTGGGCCGGTGGCTCAAATGCCATGTAG
 TGATTGAGGAGTACGTTGCCAGCAATGAAAAGCAAGAGGATTTCAAGGA
 AAAGTAATTATCCCTTATCGGWATAGACTTSKGATCARCTACAARAAA
 WARKGGATCGTTGCTTAAGTTATCRAAAAAAATGAAGCAAARAGGTAG
 GGAATWKSGCTTAATTGWTYTTGCCAWACATTGCAACTGGCGCGAG
 GTCAATGARAGGAACGTCTGGNCMTNGANTTAGGAATCNAATACCAA
 ATGCTTAANGGAAAGATTTAGCAAAGGNTTAAATACTCAGAAAATNGA
 TGCACANATTTGGATACTTATCAAAAGRCATTATCAGGGTTCGTA
 CTAGACCTGGTGCCTGRATTCGCTATTCTGAAGATGAAGAATA
 TGGCCAACACGCTTGATATTGGATTCAAAAGGTAAATACTTTAAG : C
 TGGCGGAGCTTGGTAAAGGTGTGACTATTGATTGAAATAATGGTAT
 AACGCATTATTAACCCAGAATAAATATTGAAACC : TCGTCGTATTAGTT
 TGCC : AAC : GTATCCTTTCCAGGGATCGTTATTGGATT : CC : AAGTGC
 TTTTCCACAA : CAAACATTCTACAGTAATTGAGGCAGACGCCAACMA
 AACATTGAATGAGCTACTGTGTTGAAGAAAATGGCAGGTGCAATCGG
 AACTACATGACTCTGTCAGATCAATCTAATGTTATCAATACATTAAATT
 TGTTTTTAACTGAGAAAGAGCATCAAAAGCATTACAACAATCAATATC
 ATTCCATAGCCCGAAAACACGATTGATTTTATCAGCCAGGCTCAGGCTT
 ATGAGCAGTATTCATCAGATCACTATCGGGTTAACACATTGTGAAAAGTATT
 ACGTACCAACAGGCTTCAACACATTGTGAAAAGTATTCAAAAGTGA
 TGTACGGACATAATGTATTATGGGCTCTAGAGGATGAACGCTGGATTA
 CGTCTCCTCTACCTATTGTATATCTTTAAAAAGTATTGAGGTTCTTA

FIG 15B (cont'd)

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TTAAAACCARAAAATTACTATTGTTGGAGAATTAAAGACAAGCTTAKC
 RRCGAYTGYACYYKRAAKCCWRGKKGGGWTTYGMAMRWYCKWAKSGTT
 DGTGCAACSGRATWTKRAGGTTGCGGTGTTATTARAGGCMRTGGAAGGTA
 CTYAATCCCAGTGCACAAAGCAAATGGATCTTGGATAGAAAAATTG
 TGGTCGTCTTAAAAGCCAAAAGTTCATAGTAGCTTACACAAATGG
 TCGTAGATATTTCTGAAAACCCAMCCGCTGCAANCTTGTATGAACC
 AAAGTATTCAAATGCTTACAGGGRACTTATTGATAACAGSTGSYGTGR
 AGGACTGGGTTTGTCTTYGCAGATTATTTCCAAGACATATAAAATT
 ATCTGATATTGGTGGCGCTCTGATCTTGATAAAAGAGAAAGSWTCGSR
 RATWCRGRMTYKGKWWMAATCAGGTAGTCGAGTGGCTTATGTTCAGACGG
 ATATCTGCATGAAAAGAATCTCCAATTGGAATTGGATATTGCCAAAAAA
 TATTGTGGCCCTATTCAAGGGTGTCTGATGCCGCGGGCATCATTGATCA
 GAAGACAATTGGAAAAAGTCTGAAAACATTCAAGCAGTATTAGCCC
 NTAAAATTCAAGGTACATTGATTCTGATAACGTATTGTCAGCGCAATCA
 CTGGATTATGTTACTTTCTCAAGCTCGGCTCTATTAGGTGATGC
 AGGATCATGTGATTATGCAATGGCTAACGATTGGATGGCCATGCAC
 AGTATAGAAATACCTYGGTATCTGAARGAAAAMSCAAGGGRAGACMCTG
 KTTWTTCATGGCCCGCTGGAATGTGAAAGGAATGGGATTGAATGGACT
 GGAATGAGAACGTGAAAMCARAGTTCTWTTAAGTCCAAGCGGGCAASG
 TCTATTGGACATAAAGGAAGGTTGTGAGGTTATTGAACACATTRCTGGCT
 CAGGATTATTYTCAGTGTCTGAGGTTATTGGSTGGKAGGAAAACCGNGTATCW
 AACAAATTGGGCTCACACAAAGATGTTCTNACCTCACAAGTGAGT
 CAAGGGCAGGMAGTRAWGAACWWASRRSWKMYKKRASSKSYAMYAAAC
 GAGCTGAGATAGAAGACTTTAAGTGTGAAGAATGTATTGGACTT
 AAAAACTCTGATTACAGAGCAACTAAACATCCATCAGCTCATCTGGAT
 GTAGAGAGTAATTAGCAGATTGGGTTTGATTGGCTCAGTTAGCAAA
 CTTTCCCCTGTTAAGTATTCTACATAGCGTYAACCGTTATTGGACTT
 TATTGGATATCCTACAGGTTATTGGGTTTGATTGGCTCAGTTAGCAAA
 GAACMCMCTGCGSTTATGGAGGCGTTTATCAGCAGAAAAACATYTWA
 TAGTAACAATACVCTGTCCG : TATAGTCCYTCATGTCAAAGAAAAGCCG
 CAACTGATCTAATATCATCCARC : GCCTCT : CCTTTATTGCAGATCCAT
 TGCCCCCTCAGGSTATTGAGAGTATTGATGAGCCTATTGCCATTATTGGT
 ATGAGTGGTCGTTCCAGAAGCGCTACGG : TTAAAGCAATGTGGAGA
 TTTTATCCGAAGGTAAAAGTSYGTGCAGGAGATTCTATAGAGCGCTTT
 A : ATTGGCATGAATATTATGAACACCCATCGGATGATGTTYGAA : AA : DB
 TAATAGTAAATGGAGYGCCTGCATTCTGGTATTAAAGAATTGATCCAC
 AATTGGATATCTCCAAGAGAGGGAAAAARCTGGACCCTTTCAA
 CGGCWCTTATCACAGGAATCMTSGAATGCATTGGWAAATSGCTTATGK
 WWWMYWACRCWKGMTMWTWARACRATGGGATAYKKATTGGRTTGAW
 SMAGGKTWTATMMRRYMWGMTCAATKMRGWTGACSGCACACWTTAWC
 CATMAKRMATTTTRGCATACCMGTYTGSCAGTWYTYWTTARAKYTTAAT
 GGSCMWRSATGGCWRTWAAWRCCGCWTGYTCCTCCGSYWTGGYYGCRMT

FIG 15B (cont'd)

09725938 012404

TCACCAMGCTKSCSYSAGTTACKWCARCAAGCAATKYGAWRCGSCKAWK
GWCSCGGCAGCWWYTTTRMWWYACRSSKSAWSWTKAWSGTGGSCWTGAY
SSAWGSGRGYMTGAKMYSACMWGAWGSYATAMYGAWAKACCKARNRTCAM
CSYGCCAAKSGCRYAGTGMYTGGAKAGSMWGYTGWTGCARTCGTAYTGMA
ACRWMTCTTKSGGGKTTCCAAAAGGGGTTMMAAAT

FIG. 15B (cont'd)

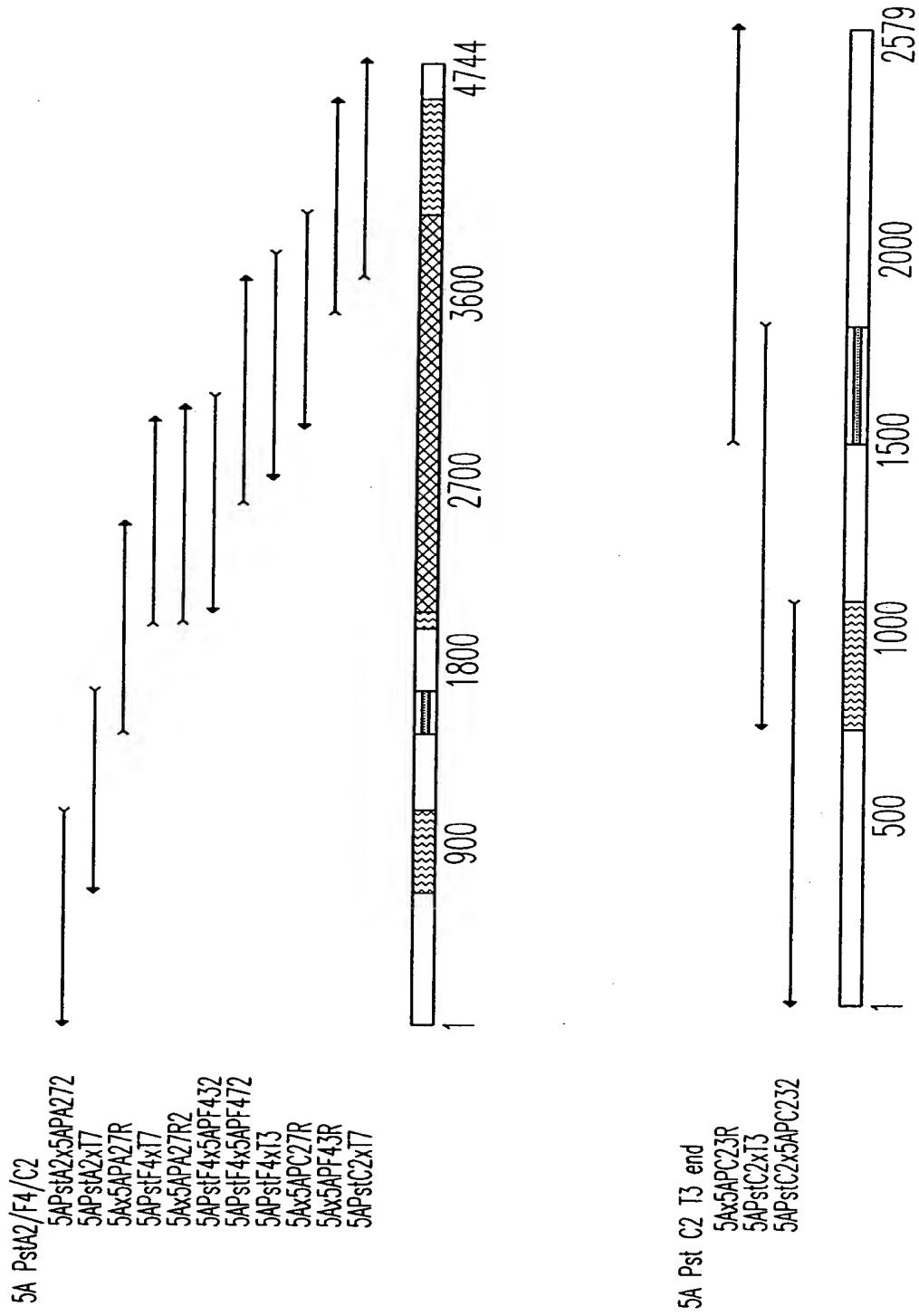


Fig. 16A

5A Pst A2/F4/C2 Overlap Sequence

GNGATGAGATTGATGAGAATACTTAATTGGTCGAANAGGCCATTACNTC
 TATGATTCTTGGTGAATTATAAGCCAATTAAACCGNTGATTAGTTGGA
 ATATGAAAGAACCGTTTATTGACTATCNGAATATTAATACTTTATCG
 AATATGATCGAGAATGAACCTCGAAGCTGTTGAGGTATAGTTATGTTAGAA
 GTTATTAAAGATACTGCCATGGATACGTATTGTCGCCAGTGGTATTGGC
 CNTAGAAGAAAAAGGGTTTGTACCTTTACAAGGAATAGATACTTA
 CATTGAAAAAATAAAACAGAATTAAATGCTAATAGTGGCCATCTCAA
 GTAGCCTTACGCATGTTGCAGTCTGTTCATGGATATCATGTGATGATAA
 AGGGTATGTACTAACAGATGCAGCGGACGAAAGAAATAAAATATCTAGTG
 ATTTTATAGAGCTTTAATTCTATGAGTCGCTATTAGAAAATATG
 GAAAGGCATGGATTAAGGATAGATCAATCCGGAGATAACTGGGG
 TATTCAAACCTGTATTAACCGATTTGGATGGTGTAAATTATTC
 CCTTATTACTAGAACTGAAGGAAATGGTTATTTGATGCGTTAAAAAAT
 GKWAATAGTCTAAATAAAATTATTTAGGNTGATATCGAACAAATCGG
 NTTCGCAAWGAAATTATTACACTATTTAAACAAAGAACTGGCTCCAAG
 AAGAATRAAGAGACGTTTACTTCACAAANTCTGGTCAATTNAYCACT
 CAACGAATTTTATTACCGCAATCCATTGCTTCTTATAAGCCATGTTA
 TCTCGGGATAACGGAATTATGTTGGTAATGCTAGGAGTATTTAAAAA
 AGGGATTGCATGGAGAGGAGGCCATGTTGACCGAACCTTAAATGTTATT
 GGTAGTGGTTTCAACATCAAAAGTACTTCGCTGATATCGAACGCGTTAGT
 CATTCAAGTTATTAATGATAMTTKACGATSRAYWSCCGAAATRKRTTS
 CRRATATGGGTTGTGGTGTGGACTCTACTAAAAAATATTTACAATATT
 ATCAAGGAAAATCTGCACGAGGAAACGTGTTGAATCACTATCCCGTGGT
 ACTTATTGGTATTGATTATAATGAAGCCGCTTGCAAGGAAACTAACAAATA
 CACTGGCAGGTGTTGATACAAGACACTATGTTTAAAAGGCGATATTGGT
 GATCCTGAAGGAATGATAAGTGTATATGATTAGGTATTAAAGATCC
 TGAGAATATATTGCATGTGCGTTCATTTCTGGATCATGATCGCCTTATA
 TTGCACCCACAGAGGTGATGAATATTGAAGCACGTTCAAAGATATTGAT
 CAGGGCGTGTATGTTGATTCAAGGTCAGCAAGCAATATGCCCTGTGGTTAT
 GATACAAAGTCTGGTGGAACATTAAACGCTGGTCTTGTGTAAAGACGA
 AACATGGCTGCTTATATTAGAAGTACATTCTCTAACCTGAGGGTGT
 AACCAATATTGGATGAAAGTGAAGTGTGATGCTTGCATTGCTATCATGG
 TTTTCCTCTCAATATTAGTATCGGCTGAGGATTCTAATATGTGCTG
 CAGAAGCTGGTTATTCTAAACCTGATGTTCTCAAAATTATCCAAGG
 AACTTACCTTTACTCGAATTACCCCTAAATTGGAAAAAGCCTTA
 TCAAATTGTCACCCGAATGAAAATGATTGTCTGCATTGATGGATTAG
 AAAAATTGTCGACCTAATAATCAATGTTATGCATTGATGACCTCGC
 CAACGCATAGATGAATACCCAAAAGGTCAATGTGTTAGAATTAAACAA
 TACCAATTGTCAGTGATTATTACAAAGTGTATTAAATAGAGTGTAG
 GCACTGCTGCAGGTGTTGGCARSWSWTGSCMDHGAATRTGBDWDCAC

FIG. 16B

TOP SECRET//SI//REL TO USA, UK, FVEY

DATTTVTABATHACTBGTATCAATDTAWTRCCAAAATAAAAAAGAA
 TATGCCATMCAATTATTACAGTTATCTTCTATYTATCATGGTGTCAWA
 ATGATGTTGAAGATGTTATGGTATTGATGAATGTTATCAGTGCTTAAAT
 GAGAAAACGATAACAAGCAGGCAGTTATGGAAAGTGAGTCAGTGATGT
 TTTATATTCCAAGAGTAGAAAAACATATTGCTAAGTATCCAATAGATAT
 TGGAGTAAATGCTCTGGATGCAGAGCAGGAAATGGGGTTGTTGGTGCTA
 AGTGGTTACTATCTATTTCAAAGCCAAGGAGTGATGAAAAATCAGGT
 GAGTATTATCAAAAAGATCAATT : GAGGTTGATGTTAAATATTATCCAA
 AATATTATCGATTATTGAGTGCTGCTACTCATATT : GAAAAAAAGAAA
 GCTTATTCAATTCAAAAAAATAC : GGTGCAAACACTTCCAATATTGAT
 GAATTGCTCTTAACGATCATTGGT : TGAGTTGCTTCGT : TTAAGCGT
 ACGTTTCCTCTCAATATGCTAGCCTATGCCGWTCTACGATTAATGGC
 ATCGTGCCTTCTCGGTATTGGAAATATTAACAGGCAAATACAGGCGC
 ATGACATTATTTCCAGAA : GGAGGGATGAATTATTGAAGGTATT
 TAAAGGCTATCAACTTCAGACTATTTAACATATTCTCGCAGAGCTGA
 TTTATGAAAGGGCTA : ACGCTCTATCCGGTGGTAATATGAA : TAAAACA
 ATTCGTATTAGAAATAAGGAGCAGGTACCTGGTGGTGCCAACAGAGTT
 TGTATT : GAATAG : AGCTTCMCCGCT : CTCGAATGGTTATAAGAGTTTA
 C : TATACTGGATATCT : CGTCC : TCGTTCCCTCGTTATGGGAGAAAAGT :
 AGATTTCYCCGATAAATAT : CCCTGGT : TGCAATATAAGGTGTTAGATAT
 : TGAAAG : CAATTAGA : TGCACAAGGGTTTACCTGATAGCTTGATA
 TT : GTGTATGCATCTAATGTT : CTCCACGATACGAAAATATACAGTAT
 ACCCTTCCCAAAGTGAGTCACATGCTAACGCAAATGGC : TTGTTAATG
 TTGAATGAA : TTTACTC : GGATGAA : GGATTGTTACTGTTACCGGTGG
 TTTGTTAGATGGCTTGGTTATATGAAGACCCCTACCAATCGATTGGATA
 ATGCTGCTGTTAAATGTTGATCAGTGGCGATCTATATTATTAAATCA
 GGCTT : AAAATGTTAAAGACTTGTACCTTGGGAAACTTAATA
 TTGAGCAAAGTCAAAGTATTATTGTCCTGAGTGGATTATGAAGACCTG
 TCTAGTAATG : TTGAAAATGTGGTAAAAATAATCA : TTGTTT : AGAAAT
 AAAAAACTACTC : TGAT : CCGATTACT : GTGGAG : AATAAAATTAG : TTA
 CAATT : AAAAGACAA : TCMCWTGTTA : CACAATAGTATTGGAAGAAAAT
 ATTTTATAAAATTAG : GGGGATAAAAAGAAAATTAT : GGATTGTTCT
 CC : TAAACGCCCTTGATTGGAGTTATGGGTTGGATTATTCGAAC
 CTAC : TTGGAA : TTAAAGATCATTACTCGGKRAGCMTTYTCYATAAAAC
 TRGAASMTACTTCKTMTKYMMAWKATKRAAYRMTKSCKMRSCTMTYTGW
 KWCMTCCSAYATSATTCMAGWTRASCYTSRWATTRTCGMRARAKWCCCTA
 TTACGGAAGAGATAATGACTGGAGGTACGTCAAGGGTAARAACAGGGCAA
 TCGAATSAAKATGAACCTATTGCGATTATTGGTATGTCYTGTTATTCC
 AGGTGAGGTTACGACAGTTGATGAGTTCTGGAAATTATTAACAGGAAA
 GACATGCCRTTCAACCCTAACCTAACGGACGTTGGCAATGCCAKAAGGT
 GTTGATCCATCGGGAGCACAACTTGGCATTGATCAGGGTGGATTCTGGA
 TGGTATTGATACCTTGATGCCSACTTCTCGTATATCGAGAAAAGAAG

FIG. 16B (cont'd)

CGGAGTTWATGGACCTCASCAGAAAACCTACCTGGAATTAARTGGCA
GGTCATASAGCATGCCGGATATAAACCCATCGGYTTTCTGGTCAAAGA
NATYGGYATCTATGTGGGTGCTTGTACCGGTAAATTATGGGAGTT
ATTTAACTAAAAGTGACCAAANGCCTAAAAACCAACCGGNAAGGCCTAT
TTKCATGACCARGTARTANATTGTTGTCGYTTMCCCCAATAANAATT
TTCCTATTTNTATTAATTAAARGTGCCTCSTCCTCTWTCTGAT
WCCNGCTTGTCAARYAGTTTAGGTTGCCTWTTGACCCAANCARTTT
TATGCGNATTCAATTGGGNANGGNGTGAATCAGGCNTCTGGTGGGNTG
GGGAYCAATTWAATRTCCCTCCSMRTGAWACCGGTTCTTNATTAYYWA
GCAGGTNTGTTNTCAAAATCNGGAATGTAAACCTTNGATCCACCGCCC
GTTGGTTTNTNCCTGGNAAAGGGGGCGCTNTCTTTTTNAATCNTT
TTCTCANCCNATTTAAAANGATTGTTTNGGGTTAAAGGGGG
AGATNAAAATNGGGGCAANCATTNNTACGGCCCTAACCTNNG

FIG. 16B (cont'd)

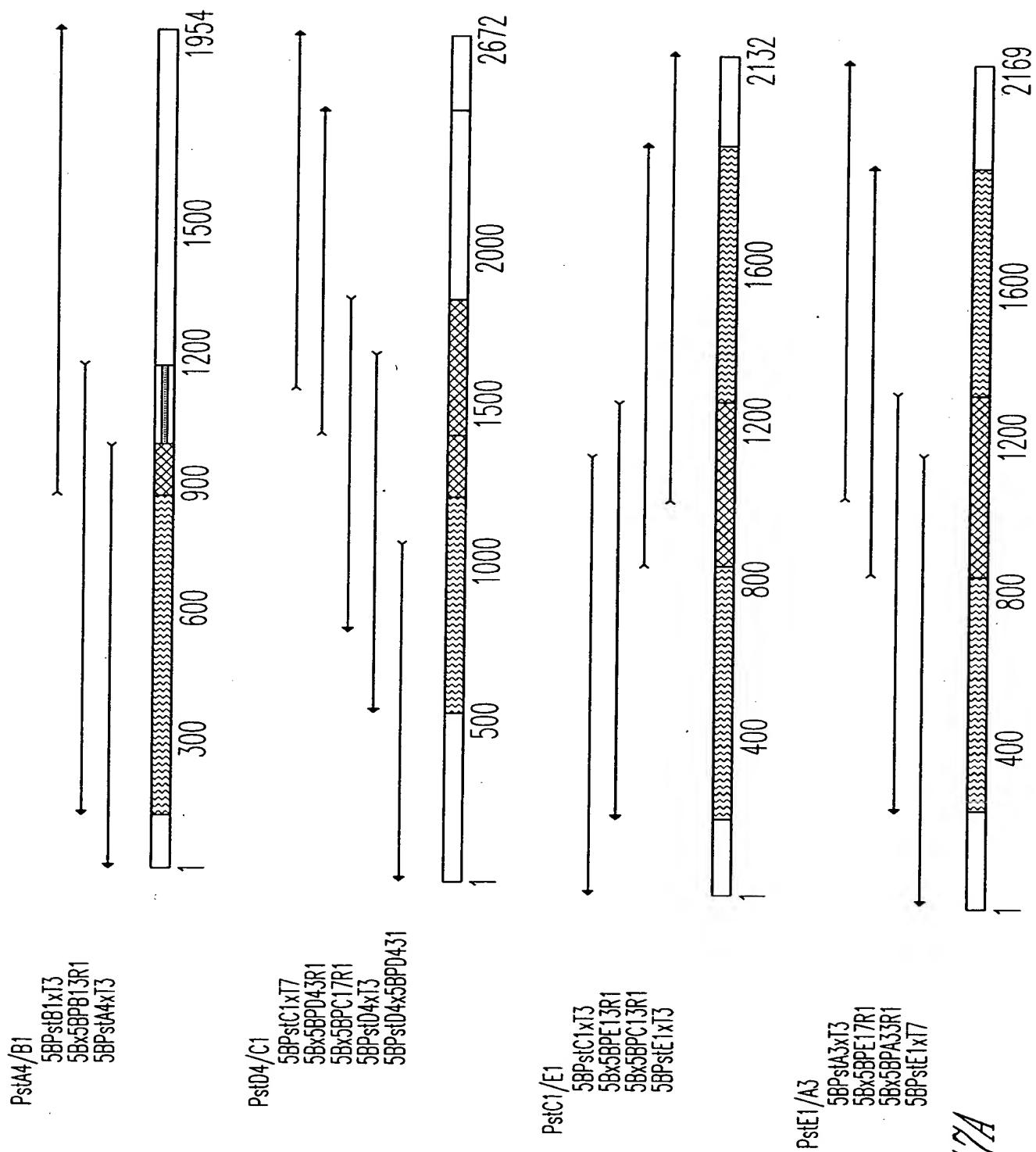


Fig. 12A

*5B PstI Fragment Overlap Sequences**5B PstA4/B1*

GANGATTCCCTNCCNCTNCCCATTGAAAAGAGGGATGGATTNGANCATATGG
 GTGTGCCTGCAAGAAGATAAGTCAATATAATGTAACTCAGAAAAATCAAT
 TCCCAAAATGAATAACCCNCAATCWATACAAAAAAWATTGAWAGATTTT
 KGGTKGACATTACTAACTTTSGAGGCNAAGACATCMATCCMRGCMGGA
 TGCCTGGTGACTATGGTGKTGATTCCATTATTAGGTATGAGATTTYTTAA
 TCGAATTAAACCYCCACCTTAAWATAGAAGCTGATGCTTATTACTAAC
 GAAGGAACGATTMACCAGTATATCTCATAAARKWCMTTCTTTATTGTTG
 ATAAAAAAAATTACCCAATGTTACCAAATTTGGATTAGAAAATGATTCT
 AATAAAGAAAATAAAGGCTGGTAAAGCCTCTTTATTGAATTATTAA
 ATTTGAAATCAATCCTGAATATAGAAAGCAGTACAAAAAATAAAGATT
 ACGCGATTCTGAAAATCTAATAAATAATGGAGTTGGAGTTGGAGAGAA
 AATAATCATCTATGTTGAGTTTTATGAAACTCATAACAAATGAAAC
 AATTAAAAAAATAGTGTTCACCCGAAATACTTTAACACTCTCTAGATA
 AAGGTAAACGATACTTCCAAGTAGCTGCCAGCAAAAAACAGTCTATAT
 CAAACGGAAGTTGAGAAGTTCCATATAATCTTATTCAAGGATTAGAGT
 GGAAATGCCAGTCATATTGAAATTAAATAAAGCATTAAATCATTGG
 TTAACACATATTCAATTTCAGAACAAAAGCAATGTTGATCAATAAGCAA
 TGGATTCAAGGTAAATACATGATGGTTATCAGTAAGATGCGAAGA : AATT
 YATACGAAGGATTATCTGCAGGAAAAAGATTTCAGCAACAAACTAAT : AG
 TATTCAAAAAGAGCAAGGAAAAATTATTGATATCGATAATCTGCCT
 TTATTAAAATTATTCCATAATGGTAAAGACTTAGCAGCTATT
 TGTCATGCGCATCATTGTGCCATGGATTACATTTCCTTT
 AGAAAAGATTTCATGATACTTRTGAAAGTATTATRAACGGANTGGRRWAT
 CCGGAAACGKTTCSAWAAAGTGTGGCTGAATATGCCACTTGCATTG
 TGTGAATATAATCCAAAAACAAGGAGCTGACAAAAACTGGCTTGATAA
 AATTGAGATAAAAATTTCCTTAAAATTAAAGATAAGAAAAGACTATG
 TCGGTCAACTGTCAAGTGGAGAAAAATTATTGAGCTAGAAGTTCTGTA
 AATATGCTGGAAAATTAAAGATTATTAAATGATGCGAATAATACCACACT
 GACGCAATTGCTATGTTGTGCTGCAATTACTGTATCGCCTCTCGA
 GGCTACCACTGACCCCTGCAAATGGTCAACAGCCGTAGAGATAAAATAGAA
 TTTGAAATAATGATGGTGATTTCATCAACTCTGCCCTATGGATTAA
 GGAACCTTCCAAAAGCATTCTCTATTCCNGGATGGTACCTTTTAA
 GTTATTGGAAAANGAAAAAGGCNTTNAATTNTCCCCCNAGGATT
 TAAANGGGTTGGATNNTNTCNGGAACCCCTAAANTCCCCATTAGGAAATT
 TTAAATTTTTAATTCCCGGGAAAATTATTNTTAAATTCCCGGAATT
 AAGGCCNAANTGGAATTAAATTGGAAAATTCCANTTGGTTTAA
 AGGGAAAANCCCANNAATTGGTTCTTAAANAAAAAAAGGGG

FIG 17B

09527263634102

GGNGGCCCGGTGGTTCTTNTGGGGNAAAATTAAAAATTAA
TTTN

5B PstD4/C1

ANCCGAAAAANACCNAAGGGNNCCGGCCNTGCTCCTNCAGTCATNA
TAAAAAAANCCAGTNATAAGNNNNACAATANTCATGCCCGCGCCNCC
GNAAGNAACCTNANTGGGTTNAAGGCTCAAGGGCATCGGTCAAGGAACC
TTTCGGCGGGCTTTGCTGTGCGACAGGCTCACGTNTAAAAGGAATAA
ATCATGGGTCAATAAAATTATCACGTTGTCCGGCGCGACGAATGTT
TGTATGCGCTGTTTCCGTGGCGGTGCTGTGGTGATCTGCCTCT
AAATCTGGCACAGCGAATTGCGCGAGCTGGTTTGCTGAAACCAGACA
CACAGCAACTGAATACCAGAAAGAAAATCACTTACCTTCTGACATCAG
AAGGGCAGAAATTGCCGTTGAACACCTGGTCAATACGCGTTTGGTGAG
CAGCAATATTGCGCTTCGATGACGCTGGCGTTGAGATTGATACCTCTGC
TGCACAAAAGGCAATCGACGAGCTGSRMCRMAKTYGKGMCMCCGKMW
CCTWMRARSTTWTCSCAAWRAGKTYWTTMAWMAAGSMCSCYGSKRKY
GSWWWTGGWRCTAWCCACGMARCSSMWWTYGAAMACCKSRKCYGGNTKW
CSRAWAWMWACMRSMYCASCCTGGWAWMMARMRWSMTGASYYWGCKCWG
AAMAAGTWACCSTCRGKGCCGMTWGKKAACWKTWMACCYSRWRWWRR
YMCMAAMATTGARRCSTTGMYCGRAACCSCGMTGAAAAA : : CGCTGH : TG
: : AATGTRVGGCGT : TGGATGTCHCAAAGCAAATGGCASCAGACAA : GAA
AGCGATGGATGAAC : : : GGCTTCCTTATGTCCGCCCCGGCAKTCATGAT
GGAATGTTCCCCSGGTGGTGTATCTGGCACCACTGCGTCGATAG : T
A : TGC : AA : TT : GA : TAA : TT : ATT : ATCATTT : G : CGGG : TCCTTT : CC
GG : CGATCC : GCCTTGTACGGGGCGCGACCTCG : CGGGTTTCGCTA
TTTATGAAAATTTCGGTTAACGGCGTTCTGAAAGAAAGAACGACAGGTG
TTAATGTTTATTTAAAATACCCCTCTGAAAGAAAGAACGACAGGTG
CTGAAAGCGAGCTTTGGCCTCTGCGTTCTCTCTGTTGTCC
CGTGGAAATGAACATGGAAGTCAACAAAAAGCAGAGCTATCGATGATAA
GCGGTCAAACATGAGAATTGCGGCCGATAATACGACTCACTATAGGGA
TCATATTATGGTGTATTAAAGGGAGTGCATCAATCATGGTGGAAAAA
CCAATGGCTATAGTGTGCCTAACCGATAAGCAACAGCGTGTCAATTAGT
GAGGCTTGCAGCGGGCTCAAATAGCTCCTCATCAAGTCAGTTATGAGA
AGCGCATGGTGCAGGGAGCCGTTAGCGACCCAATAGAAATTACGGCTC
TCAGCAAAGCATTAAACAATGTTAGTGCAGCAATTAAATGTGAAAAGTGC
GCCAATCAATCGTGTATTGGCTCGTAAATCCAATATAGGAAACTG
TGAATCTGCAGCAGGGAC : TGCCAGTATTAGCAAAGTATTGCTACAAATG
AAACATGGGCAAATAGTGCCTGCATTCAAAAGAACTGAATCCCAA
TATTGATTTTCAGCAACTCCCTTGTGGTTAACCAAGAACTGCGCGATT
GGCAGAGACCGCTGATTGATGGAAAAACAGTGCCGAGAGTTGCGGGTGT
TTTCATTGGGGCAGGTGGTCCAAT : GC : TTACGTGGTATTGAAGAG

FIG. 17B (cont'd)

TATATTGCGAAGATAACGACAAATAACACCAGGAATCTATAAACCATAG
 GTCTATTATTCCATTATCAGCACGAACGTGCTGAGCAGTGCAGGCAAATTG
 CCAGTAGATTGCTGGCATTATTGAAAAGAACAGCAAGACAGCGTGGTT
 ACCCCCCTTAATAGATATTGCTTATACATTGCAGGTAGGACGCGAAGCAAT
 GGATGAACGCTTGGGTTATTGTGAGTTCAACCCGATGAATTAGTCGA
 GAACTACGAAGATATCTTCAAACACACGATGATATGGAAGAGCTTATCG
 AGGTCAAGGTTAACGATATGAAGACACCTTCTACTATGGCGGCTGGAT
 GGAAGATCTCTCTGAGGCTATCCCACCCATTGGGATTAAAAACGAAA
 AACTGGTCTTAAGTTAACGCAATTATTGGGATTAAAAGGGCTTT
 GTGGATTAAWTTKGGRKRAGWTATASSWTKYTTMCAAARGRKGWTW
 KTCCYCSGCRMATKARMKKAYTACCTRCCYTTYGGCRGSMATATTTTA
 RGWTKKTAMMSWTYRNMCCTCWTWCCTYTTTGTGRCCCCAGGGNCCAAA
 TTTATTTNGTTGNGGGAAATTNGTTAAAAAAGAATCGGTTAANC
 CCACCTNCCNTAAACTTCATTGGGGGNAATGGGTTTATTGGNAA
 CCCATTCCNAAAACCAAAANGGCCTTTTTCCATTCCNAAAAAA
 ACCAAATTGGCCCTTTTGGGGGGGAAAAAAACCCNAANGG
 GGAAAAATTNTTTTAAAAAAA

5B PstC1/E1

NNNANNTTCCNATTCCCTGGCGGAAATTGGCCAGGGNCCGNAT
 AACCAAAGGACCCTTTTCNGGCCCTTAAAAAACCAATTNCCCCNT
 TTAATCCCCCGAATAAAAGAACCTTCCCAAAAAGGGNAANTGAAN
 TGGGGGNANCNTGGAAATCCAAGCCAAAAAGGCCAAYMTCGCC
 WARAAKRKKCCAWWAATSSSGAWAASMCYYCCAGAWARWATTKWTKRRWA
 MWRAWCYAGYWWMSCAMATCRGRTGTTWTATGGRRSSRGWMYAWWTRA
 AARYMYTCCAwyKTKTTKSSGRRTCAATKATGSSRKWTYYTCAAYMTTGG
 GACTCMCYYMTCMMWWTTGAAAACCMYWATTATAKKTRTAAGSGGGCC
 AAATAATCAATGTTGGATATGGTAAMCCGATAAAAAAGCCTCAATAA
 ATTTNCTGCCAACAACTAAGACAGCTCTACAATAAACATAAAAGCAATA
 ATGAGTCCCTGTGATTATTCCCATGAAAAAAACAATGGCATTAAAGT
 ATAGATCTCATACTGAATCGAATATTGCCATTATAGGTATATCAGGGT
 TTTCCGGATGCAAAAATGTTAATGAATTGGAAAATTAAAAATGC
 TCGTCATAGTGTAAAGAAATTCCCTATAACCGGTCTGGATATTGATA
 ATTACTTGATACTCTCGAAACACATGCACAGGAATATGTTAAACAA
 GGAGCATTAGAAAATCGATCTTGTGATCCGCTGTTTTAATAT
 TTCTCCGGTGGAAAGCGATTGA : A : GATGCTGGTTATGATGCATCAA
 AGGAATCCTGGAAAGCGATTGA : A : GATGCTGGTTATGATGCATCAA
 : TAAGTGGAAAACG : T : TGGGGGGTATTGCGCTGTGCAAAGGGAGACTAC
 CATGCCATTATTACAAGCAGGATAAAACTCGTATCATGACCACTGACTC
 TATGCCTCCTGCCAGGTTGCTTATTGAATTG : : TTAGGGCCTGC
 AGTTCACGTTGATA : C : GGCTTGGCAGCAATTGCTT

FIG. 17B (cont'd)

ACGCATGTGATAGCCTCATCTTAGAAATTGTGATGTTGCCATTGCAGGA
 GGTGGAAATATCAACTCAACTCCCAGCCTTGTATGCCTSDATCAACGTGCAA
 TGGTTGTTGTCAAAAGATGGCGATGTTATGCCTSDATCAACGTGCAA
 ACGGAACGGTATTAGGGAGGGCGGTASCATCGATTATTTAAAACCTTA
 CAACAAGCGATTGACGATGGTATCAGGTCTACGGATTAATTAAGGGTTG
 GGGAAATGAATCAARATGGAAAAACCAATGGTMTTACTGCTCTAGTGTG
 AGTCACAAATTCAKTTGGAAACGGATGTTATCAAAAATTATGATWAAT
 CCTGAACATATTACKATGGTSMAGCCATGGAACGGACTAAACTASG
 AGATCCCATTGAGGYTCAGGCATTAMCAGAAGCTTTCASAAATATACTY
 AAAAAACAKGGTMTTGTGCACTAGNGTTCTTRAARWAAATATTGGAC
 ATACNTTTTCCCCTGCTGGRAKTCKTAGATGTTAATMAAGGGTTTG
 TTGTCCATTTCWCANCATTYACMARGWTTCYTYCRTARTWWTAATTYW
 MAARSTATNAMTTWTTCAWWATTCTATYGTNAAWWACCCYWATTTKKW
 KTAAMCAGCYCATWWTTWYYSSSKGTMATTWWNYCCNCTTWTTRW
 WMCCCCMMYTTGCGRCSGTTTTCTGCKKTGTTCRWCAKAGAATCTM
 MMSYCCCTTTTYGCMMAANMRNNTTAAACMMMTWRCCCTTYTTTRGR
 KGGSGYCCCCNCCNGGGGAANCCCCAANTGGTCCCNNTTGGG
 GGGGGGGNTTNGNNAANGAAAAATTCTTATGCCNNANAAAAGG
 TCCTTCCGCAACCTTTAAAAATAANCCNTCCCNAAAAANTGGG
 NATTTGGGANTGGGAATTAAAAAGGCCCTTTTACCCCCCGNGTTA
 ATTTAATTCCCCCTTTTGGTCCGGGCC

5B PstE1/A3

NNACCAATTTCGAAACCAAGNCATTTGAAAGGGGTTTGGGGCCC
 GGGGTTGAAAAAAANGGGTTTTGGCCCCCCCCNNAGNAANTA
 AAAATGGGTAAAGGAACNCGCCCAACTTGGAAACCTTCCCCNAAA
 AAAATAAAAGGCNTTGGAAATTCTTAACNAAATNNCGGGGNTGGC
 CNTTAAANAAACCCCCCNTTNCAAAATGCGARRGGKGGYCTCCWR
 RNAYTYYAAWAWGRAMGSGKTAWYTMCCWAKTGRGGGWNTWTATCAWT
 AAAGGNSSGGGKTYTAWKWTAAWRAARRGGRAGCTTAGRAAWAWAAW
 ARWCMGPKGTTAARAGARATTKWWAARRRAACTGGRWTRAAKTWWWW
 RWRTTATWATANAAATRKWAAGGGWRTATAGAGGGAAAAATTAAAG
 GGATAATGAARGAAACCCATCWCCATTATTTCCAAGASGACAAAGA
 AATGATAGAAGTTGTTAAATTATGGRTGCGTAAAAAGAAATTCCCAA
 AWTTTAAWYCTTGGTTAAAGGATTAACMCTGRTTGGAAAGCAATT
 ATATGGTAAAGAACMTCAGCTCGTATTAGTTGCCAWGCTATCCTTG
 CCAAAGAGCGGTATTGGTGGATACTGATAAGTTAGTCGACGGTAGTTA
 TYTCACCCAGRCAAGAGGAATWAATACAGATAGTGATAAGTTGATG
 AAAAGCTTATGAATCCTGTTGGACAATCTTTCCAAAATATGACM
 CCTGATGAAGCTATTAAAGTTAATGGAAGAGGAGGTATCATGAAAAAATTA
 ATTAAATTGATTGAAAAAGTTTGAAGAAACTATCAAAATCAGA

FIG. 17B (cont'd)

FOURTY-SEVEN

AGCCTTGTGTTGATTAGTGGATTGAAGGCGAGCAATACTACTATCCTTC
 ATCCCCTTATAACATGAAAACACGTCAAGTTTTGAAAAAAAATTCAGT
 TCAACTTTCTGGTAGAGAATTTCTTCGGATAGATGCTAACCTAA
 AAAAAGTGTATTATCTCCTGTAACATACCTGAAATGGTTATGCTGCAG
 CAACAAAGGCAATGGCTGGTGAGAAATTCAGCGCAAT : TTAAAAAAAT
 TGAGTGGCAATATCCAGCTATTGTTCATGAAGAGTCGATAACAGTCATA
 TTCGTTTTAAAGATCCAAATACCTGGTTGGATACAAGTGAGGAGAAA
 TTTTATGCTATCAAATTACACAATTCAAATAATCAAGAAACA : A : GC
 GATATTGTTACAACCGGGGTGTAATAGATTATGATCATAAAAATAGTGA
 ATTAAGTCCACTTGATATTTTCACTACAAAAGCATATCAGTGAATATT
 TTCTAGACCTAAAGAGGATAGTGAATTTTGAAGAGCGATAAAAGT
 AATGAGCCCTATTATCAGAGTATTGAATTGTTACATATTAATTTCAGAA
 AGAAGCGCTTATAAAATTATCGTTGATCAGTACAGGATACATATAAC
 CATCAAGAGTCATTGGTTTACATCCAGATATACTGGAGTTGGCTTACA
 ATCCTGTAGCTTCTTATGCCTTGATATGGCAGATACTGGAATCTGAGTT
 TTCGGGGGAGTTGCAGCCCAGTGAGTGGTAGATGCTTTATCAAATNCAT
 GTCTCGGCTGGTCCAGGGACCTCAAATGGTGGKTTGGTTACCGGCTT
 AACARSYTTCCATGGAAGGGTAGGGNTTAWATAGSRCRCANTATGGCCY
 TKGGTGRGTTGAATRAWRGTWATKCSKGGGGWCWGSTMWWAGGGTTGGG
 TTYTCAAAACCAAWRAAMMSKGTTTYYTTGRRKWWTTTTSSMMMGCC
 SCNAAATTNGAACCCCCNNNGNTAAANCCCNGAAATTNNNTTTTT
 TTTTNCCCCNNCCCAANCNNAGAAANGAACCTTNCNGNGTTTGGG
 CAATTAAATTAAATTAGGGCAAACCCCCCTTAATNGGAAGGGGGNCCA
 NTTGGGNGGTTTTTNGGAAAAAGGAAGGGNAAATTGGGGNAAAAAGG
 CCCCCCAAANTNGGTTTAAAGGGAAAAAAATNAACCGTTAA
 AAAAATTNNCCCCCAAANT

FIG. 17B (cont'd)

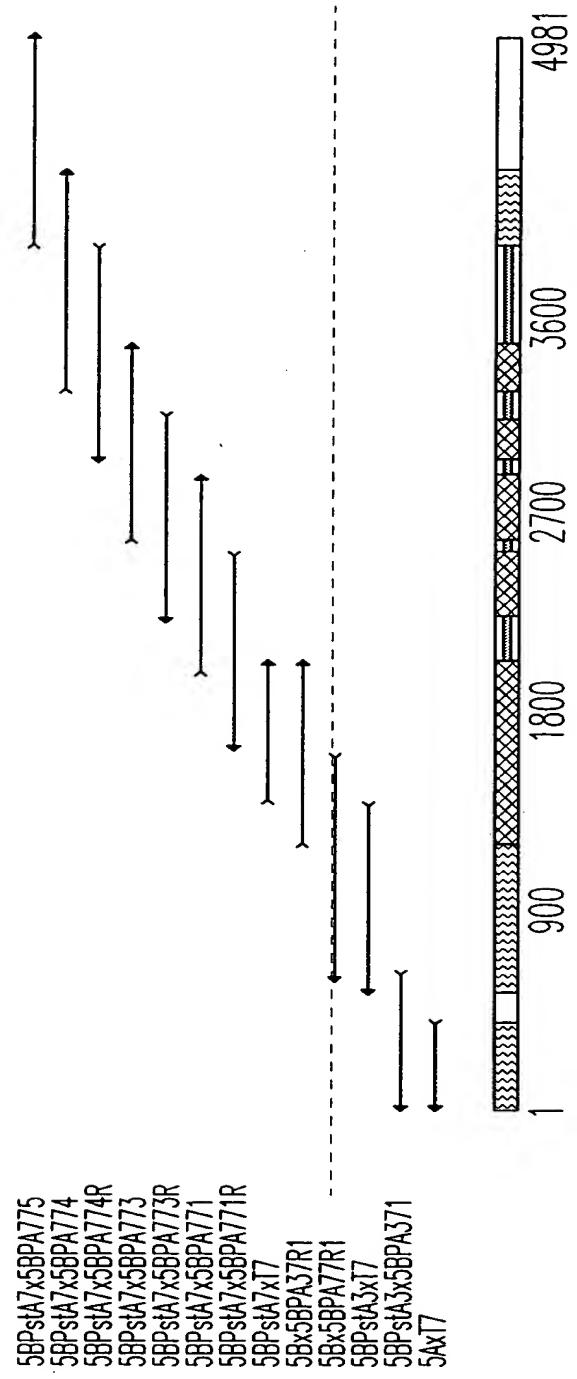


Fig. 18A

5B PstA7/5A T7 Sequence

GCACCGTTGGAACGTTATGGCATCGATTGATTGATTGATTCAAGGTGAA
 TCAGGCCTTGGCGGCTATTTGATGCGCTGCCTAAAACACTGTTATTTG
 AATATCAAACGATAGACGCGGTCGTGGCTACTTGGTTGAGCAGCACCGC
 CAGGCATGTAGGGTGTGGACGGGTTAACGGCAACGGTCAAGCTCAAAG
 AGAGGGTGTCACTCCCTACCTCATCAGCGGGTGTGAACCTGTGACAC
 CGAGACAGAAAAGAGGGTACCTACAGAAAGACATCAAGTGCCAGAA
 CACCCAGTGACAGACGAGCCTATAGCCTATTGGTCTGAGTGGACATTA
 TCCGCAAGCGAATAGTTGGATGCGTATTGGAAAACCTGAAGGCAGGAA
 AAGATTGTATTGTGAAATTCCCGATGACCGTTGGTCGCTAGACGGTTTT
 TTCCATGAAGATGTTGAAGAAGCGATTGCGCAAGGGAAAAGTTACAGTAA
 ATGGGGCGGTTTTAGAGGGATTGCTGATTTGACCCTCTTTTTA
 ACCTATCGCCCGAGAGGTGATGACGATCGATCCACAGGAGCGTTGTT
 TTACAGAGTGCCTGGGAAGCTGTGGAGGATGCCGGTTATCGCGTGCAG
 CTTGCTTCGCAGTTAACAAAGCGTGTGGGTGATTGCGGGTATTACCAA
 GACGGGTTTGATTTTATGGAATAACATCGGATCSAGTSBTYT : YCGC
 WT : ATACTTCCT : TTACKCCAGGTTAAAARGCCWMGWTCAAGCT : TKT
 TSGGGTTTTAABTHHCGGGKGGT KTTT KVSCCVWAT : AGCA : CSG
 DCGGTTTTKMATTTTTAWTGGRAA : AC : : CAATCGGGATCAAC : TCT
 TT : TCCGCTTATACTTCCTTAGCTCAGTGG : : CT : AATCGTGTGTCTTT
 ATTTTTGGGTTACAAGGCCAAGTC : TGT : CTATTGATACCATGTGCT
 CCTCATCTTGACGGCAATACATGAAGCCTGCGAGCATCTGCATGCCAA
 CGATGTGAAGTGGCTATTGGGGGGAGTGAATCTTATTG : CACCTT
 CAACCTATATTAGATTGTGTACTTACGGATGCTTCAAAGAGGGCCTG
 TGCAAAAGCTTGGTTATGGTGGTAATGGTTGTACCGGGAG : AGGGGG
 TTGGCGCTGTGTTGAAACCCTG : : TCTAGAGCCATTCAAGGATCAGG
 ATAGTATATATGCCATTATTAGAGGGAGTTGTGTTAATCATGGTGGCAA
 ACCAATGGTTATACTGTGCCAATCCACATCTCA : AGGCGATCTTA : TT
 CGTGAAGCTTGGA : TAAAGCTCA : G : GTTAA : TGCCCGTAT : GGTCA
 TATATAGAACGCC : CATGGTACA : GGTACAGAGTTGGGTGACC : CAATAGA
 GGTAAGAGGCCAACGCAAGCCTT : TCAACAAGATACTGATGATGTTGGT
 TTTGTGTAT : TGG : GTTCAGTTAAATCTA : ATATTGGTCATC : TGGAAG
 CTGCCGCTGGTATCGCTGGCTGAGCA : AAGTTATTCTGCAGATGAAGTA
 TGAAAAAAATAGTGGCAAGCCTACATGCAGAAAGACTGAATGCCAATATAA
 ATTTGAACAAACTCCTTGTGTTGAGCAATCACTTAATGAATGGGAA
 AGACCAAACCTCATGTTAATGGAAAAATCAAAGAATATCCTAGGACCGC
 GGGGATCTCTTTGGTGCAGGGAGGGAGCAATGCACATATAATAAC
 AGGAGTATATTCCAGAAGTCAGTCAGACACGACAATCAGAGGTCAAGGAAT
 AAACCAGCTCACCCGGTGGCCATTCTGCTATCTGCGCATACTCCGCTCA
 GTTACTGAAGATGGCCGAGGCACTTTACTATTTATTGCGTACCATAGTGA
 ATAATATGGACTCATCCTATTGGCAGGGATGAGATGACTCACTTGGTA

FIG 18B

AATGTAGCCTATACATTACAGGTTGGACGTGAAGCTATGCAGGAACGCCT
 GGGGTTTGTGTGAATTCCCTGAGTGATATTGAAGTGAACACTACAAAAAT
 TTATTGATAAGGAAAATGATATTGAAGACTTTATCGGGATCAAATCAAG
 ACTAAAAAAAGAAATCTCAGCTCTATTAATTGGATGAAGAGATTGCAGGA
 AGTGATTAACAAATGGATGCGACAAAAAAACTATCCAGGCTTTGTAC
 TTTGGGTTAAGGGAGTTCACTGTGATTGAACTTCTGTATCAACATATG
 CGAACCAAAACCTTATCGGTTACATTACCAACGTACCCATTGCTTATAA
 TCGATATTGGATTGATGATAATAATAAAAAATCAATCGACTGTAGTTGAAA
 AAACCAACACTATTATTAAAGAGAGAAAAGAGCAAGTTAGATTAGAGCCG
 CTTGATTTATGGAAAGGAAAAACTTAATGTCCATGAAAAAAAGCCATT
 TCATTGTTCTTATCAACTCAATCAGAGGCCTGGTCCGGGCGAACACTC
 AGACATCCAGTGGTAAACAAAGACGATCTTATGTACAGGTGCTTAAACAA
 GACGATATATTAAGGGATCTTAAATCAGCGCTGCCTACAGCTGTTGAAGG
 TATGATACCAACATTAAGGAACTGGGTGTCATGACAGAAAGCTTAAAGCT
 CCTACTCAGAAGCATTGCAAACATGCTGGTATGTGTGGAGAAGTA
 TTGGACTTGGGTGTCCTATGGAATTGCAACGATTGCAAGCAGCTGGAGCG
 AGGGGCTCAAGTATTAGCCGTAGATATGGAGGCACAGCATCTGGAATAT
 TATCAGACCGTATTGGATGAAGTGAAGTCGCGTTATCGACACAAGTA
 GGCAAGTTGCTGGATCTTCATTTGATCAAGAACGTTTGTGCGATCCA
 TGCGAGCCGAGTGCTACACTTTAAACCCACAGGATTCCAGCAAGCAT
 TACAAAAAAATGTATGGCTGGTTAAACCCGGAGGAAAATTATTATTGTG
 ACGGATACCCCTTATATGGGTATTGGCGAGCAAAGCAGGGTTTATGA
 AACTCGTAAAGCAGCAGGGATTATGCCAGGCTACATAGATAATGTTG
 GTTCTCACTTAATACTAAAGAGATAGAAGGGCCCCACTCTGATCAAC
 CCGATGGACCCGGAAACTGCATCGTAATGCAAAACATTGGTTTCA
 TGTAGAAGAGACTGTTTTTGCAAGGAGAAGCCTTGCACAAATAATA
 GTTAGAAAAATCAGGTAGAGAGCATGTTGATATAAGCATTGAAAGCCG
 GAATTGGAAGATTCCGACAGGCTTGAGAAATCGCTATTGCCAGTACGGAA
 AACTGAAACGGAGAATAAGGAAATTAGCCTACTGCAAATACAGACAATGC
 TTAGGGAGAGTCTTGAATTGAATTGGATATAGAGCCGGTATGTTGGAT
 GAGTTAAAACCTTTACAGATTTAGGGTGGACTCGATAATGGAGTCAC
 CTGGATACGAAAATCAATAGTCACTATGGATTATCTATGACTGCGACGA
 AAGTATATGATTACCAAATATTGAGTTGGCAGAGTTTAAGAAAA
 CAAATTATTCGAATGATGAAAAGCAGCATCAACCCTATATCAACAAAT
 ATTTCCCACTTCATTGGATGAATTATTGAAAAAAATACAAGAAGGTACTT
 TAGGGATTGAAGAAGCCGACCAATTAAATTGATGAACTACCTGATTACCAT
 CTAGATATGGAACCTCATGAGTTGTTATAAGGGAAAGCGAGGTATTGG
 TGTCACACCGATGGATGGTAAACCAATTGGCTGAAAGAATTAGCTC
 AAATCGGCGCAGCTTGTGCGTCCGAGTGATTGACTTGTATGGTGA
 CTCAACTATGCTTGTACGGCATTCTACATAAGTAGGTGAAAATGGA
 ACAATTAGTGTAAACCAATTAGAGACAATTGAAAAGTTGTAGAAC
 AAGCAGTTAGCACGCATGAGCCAATTAAAGTAACGCGCAGAGCCAGTGAG

FIG. 18B (cont'd)

GCTTCGTCGTGATAAGTGCCGATGATTGGGAGCAAGAACAGGAAAGCCT
 TTATATTTTCAGAATAGTGATTTGATGCAACAAATTGCAGATTGCTTG
 GTACGCATACTCAGGGCAAGGGATAACAAACCAACGGATAATGAGTTGAAT
 GAAATCACTGGTGCTTGAAGGCCATACCTGGAAAACGGAAAGCTTT
 GCGAGCAAGATAAGCGGTTACACAAGCGTTATGCAAACACTCAAAGAA
 ATGCTTCACTCGGAAGATCTAACCTCCGGATTAGGTAAACCTGAGCCGCT
 TAAGCATAACTTATCTGGCTTATGGTCTCGCGCATTGCAAAAGACC
 GACTGATATATCGCTTATTTCGCTATCGTGGTCACTACGATCACAT
 TTAGTTGCCATAACGCCATAACAAGGGAAAATATGAAGCGCAGCGGAATC
 TTTCCCTGTGGTTACGCTTGTATAAGGTTGTTATTCACTTAGACTC
 CCTCTGTGTTACTGCAYTGTGTGGTAGCCAGTCCAGTCCACGTTTTG
 KGGGCSRWTTCATATGTGTTACACTAAGGAAAGCTGGTCTGATTGTT
 MCCAMCCMCCATTGTATATTTTAACTCAATGGATAAAATGTTTATA
 GCTAACTGTGAAGCTTCGATTGCCTGATTGAACTCACGATCATTTC
 TGATTTTCATAAAAGGCAGTGGTAGGTGAAAATGAAGCTGGTCTGATT
 TATGTACAGCTTATTCTGAATCTAATTAAACTTCATATATTGATAT
 GCTTGCTTGTGATTCAATTCTTCCAGTAATAATTCTGTGCAAAC
 TAGCCATTAGAAATAATATCTAATTCTAAGTGCTCAACAAACGTAT
 TTGTCAGACAAATGACGAGCAGAAAATCWTAGACTGTATATTCTAAA
 TACWTAGAGGACAATTWTCMCACAAAAGATWTCTTGCCTCCACTGAGGCT
 ATTTCTTYTTGKAATCTTATCCCTAATATTTCCCAGCTTAGTGACCA
 ATAATTTATATCATWMAGGTACTCTGTAAGCCGATAATACCTTGCTTA
 TATCCAATAATTGGGACCAAAAAAGTGCAAAAGCGTGGCGCAGATCG
 AGAAATTATTCCGTTGYGGAATAGACTATTGCATCAATTACTGCTCAA
 WGCGCTGAAAATTCTGCAAATTGTAAGGGCTTACGTGTTGTCTT
 GTACAWAGCTGTTCTATTCAAGCAGGAGACAAACATGGATTAGCAAGTATG
 GGTGTAGTTATCACTKAAAGAAATCATTGGCAGTATAGTCAACTCATTGA
 AAGTCCTATATTAACGTCGCCGAAAGTTAAATAGTTTACGATGAGATG
 TAGGCATTGTGATAATGTGCTGCACATCATCACAAATCATTCAAGCATATC
 CATAAACCTCTCGAACATCTAACATCATCTCCGTCAGTGGAGTTGTTG
 TTTGAGGAATAATTGGATTTCGTCGACATCRRACTGAAGCTTCAAAG
 GCTTCAGATAACGCTTGCTTGGCCTTAAATATTCACTGAGGAAACCAG
 TACGCTGATCTTACCGTTTGCTCAATATCGGTGACATCCACATT
 CCATCATTAATGTCTCCAATACGACTTCTCGTCATTCCAGTGAACAA
 AGGATTGCACAATGATTAAACATATGGCTAACACTGCCTGGTACCAAT
 CTTGCTTTGGTTGGTAAACAAATACGCACATCACCGAAGGTGCGAT

FIG. 18B (cont'd)

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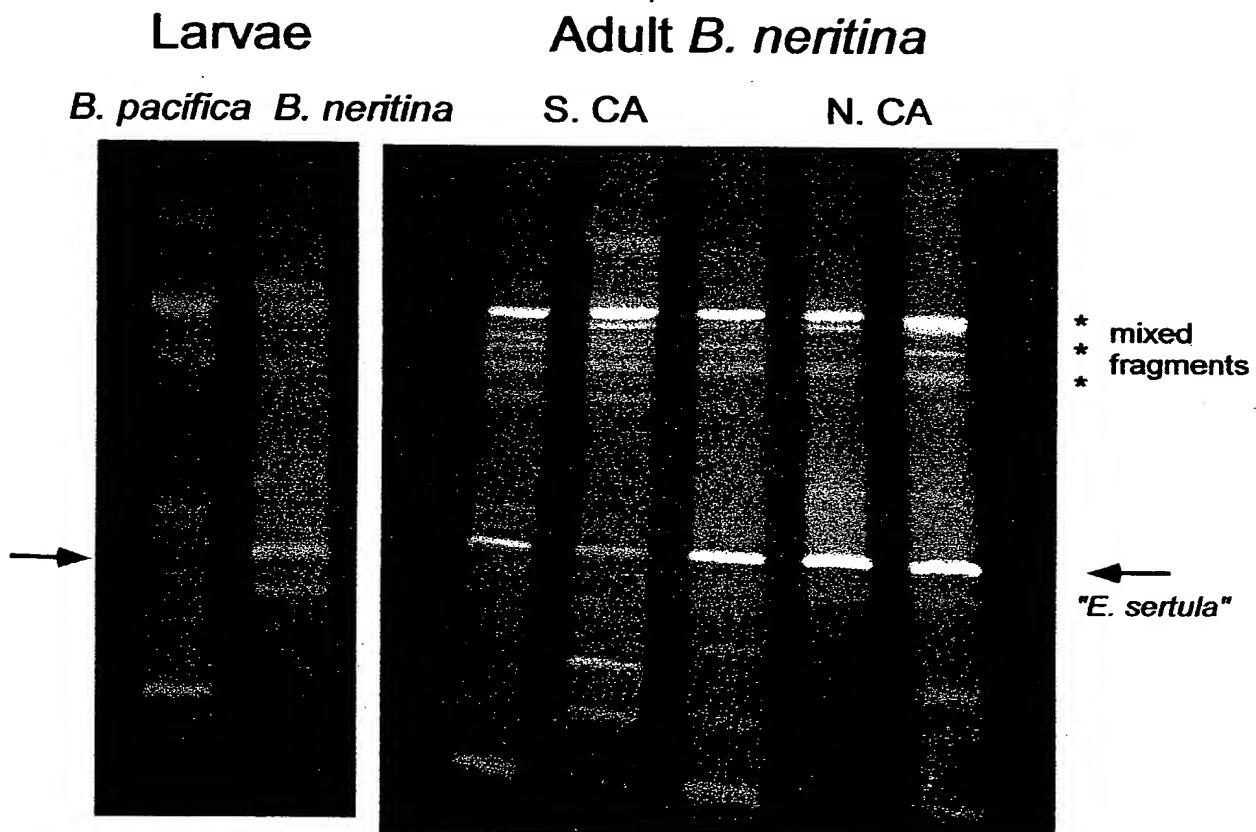


FIG. 19

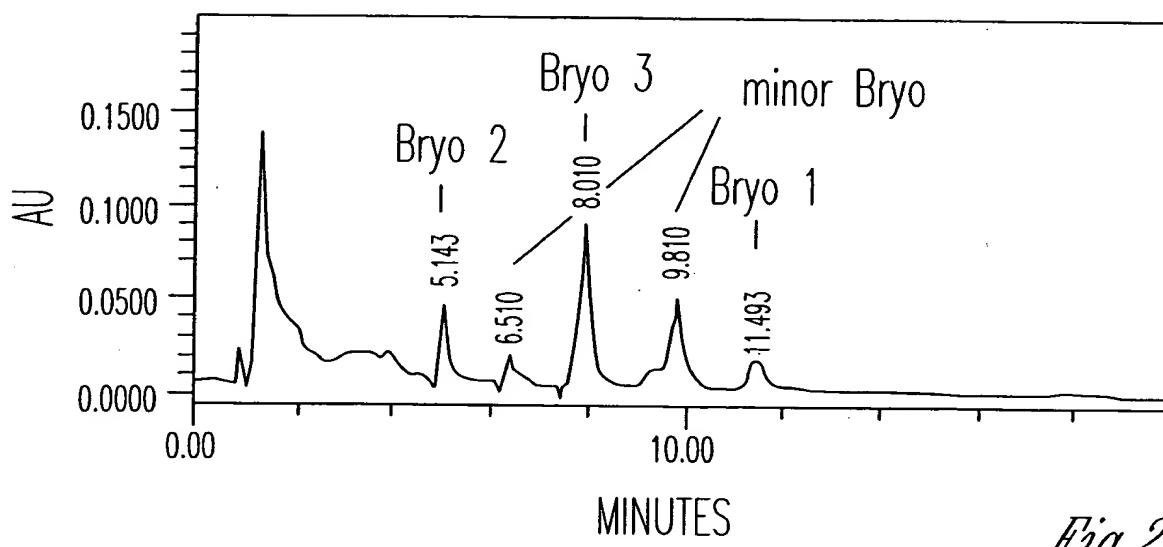


Fig. 20A

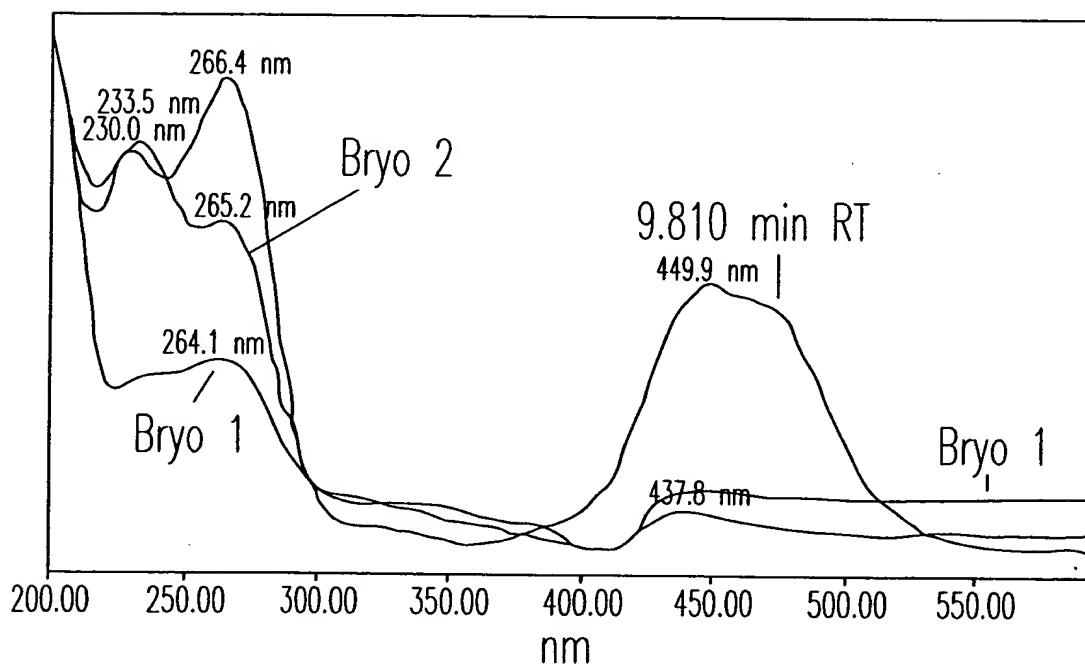


Fig. 20B

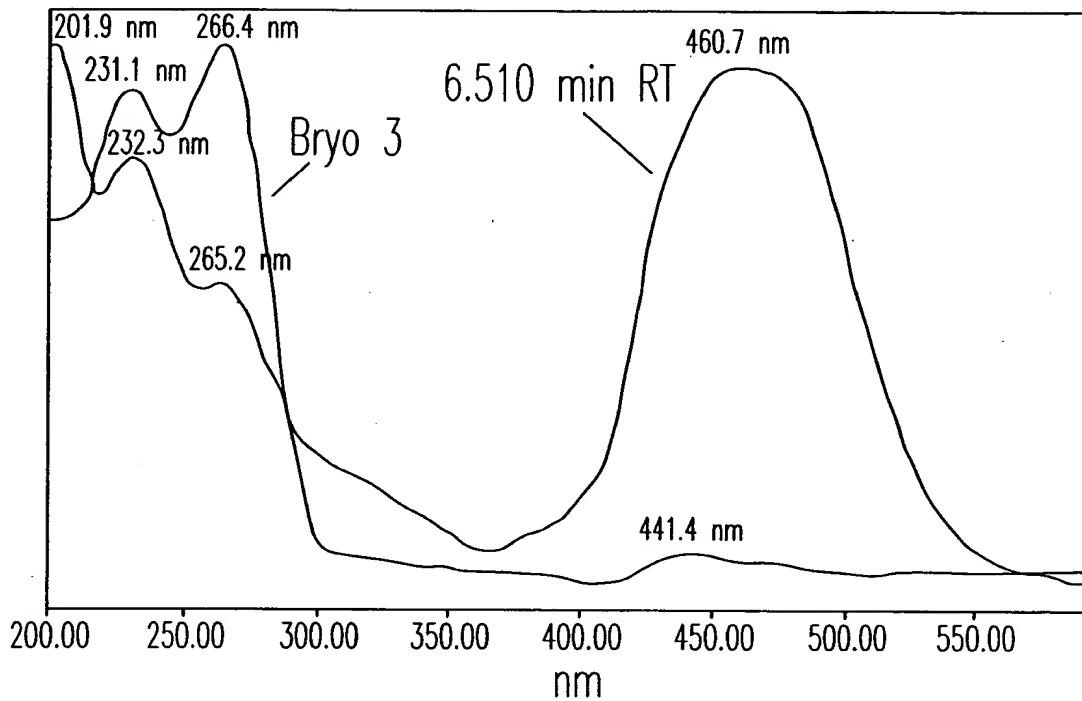


Fig.20C

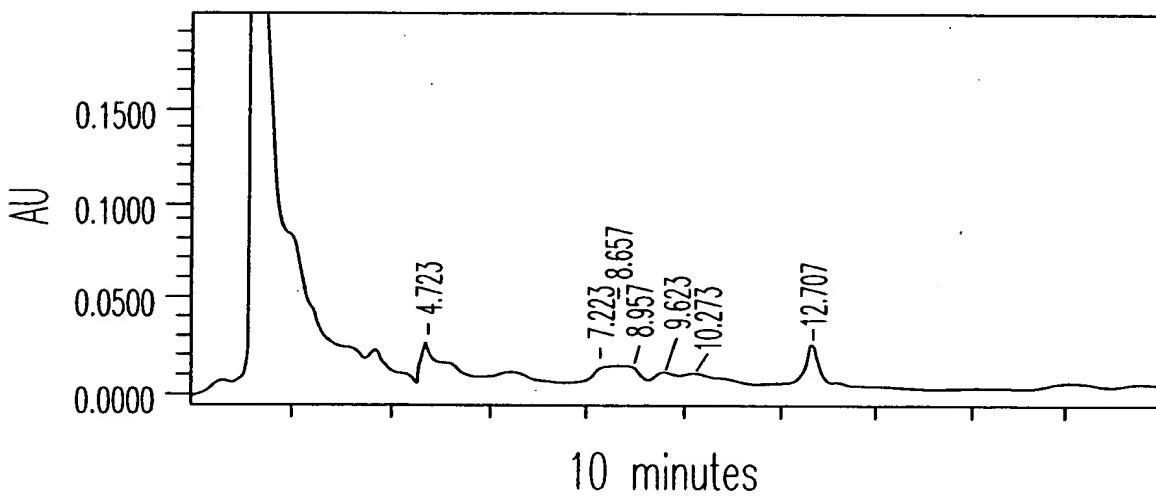


Fig.20D

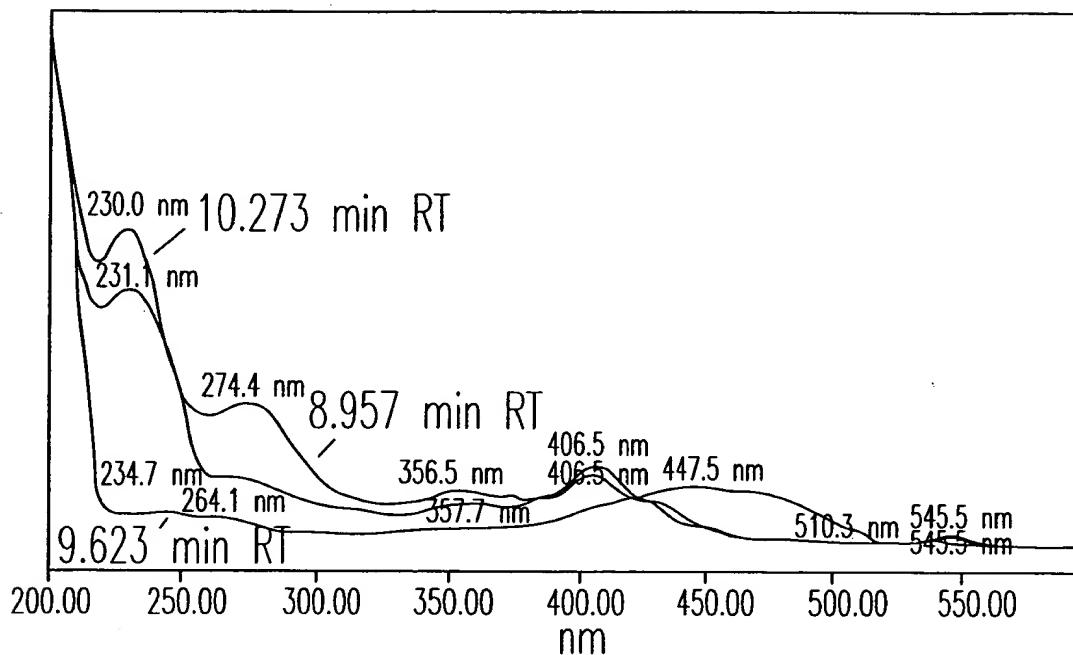


Fig. 20E

FOTOFED "SPECTRA 2000"

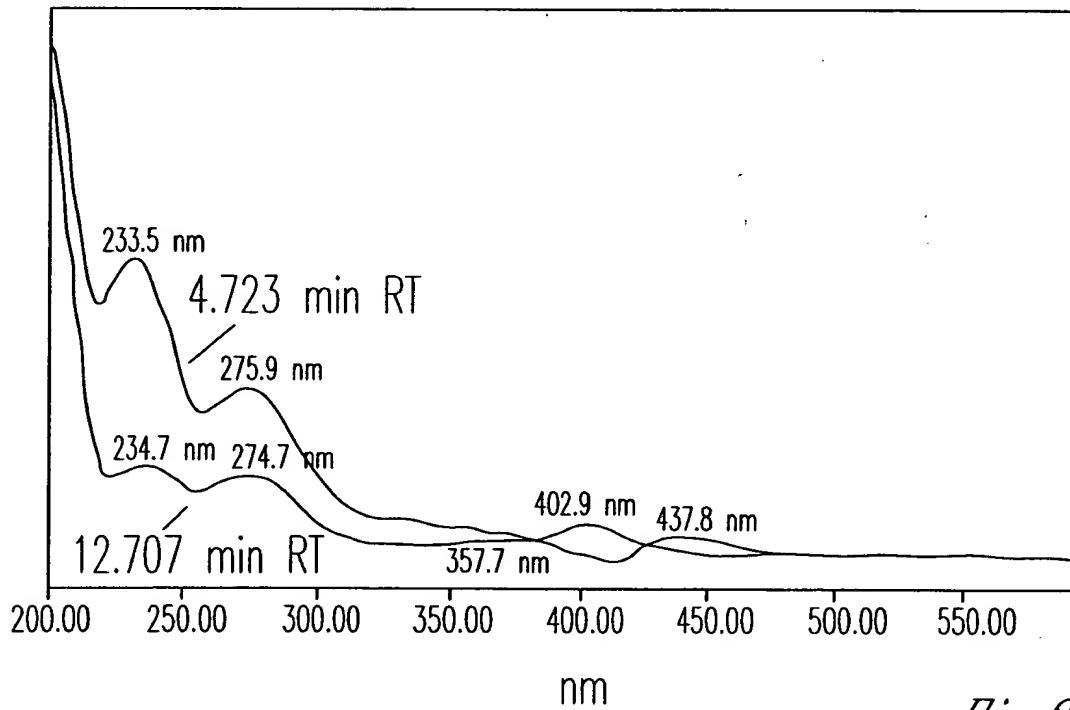


Fig. 20F

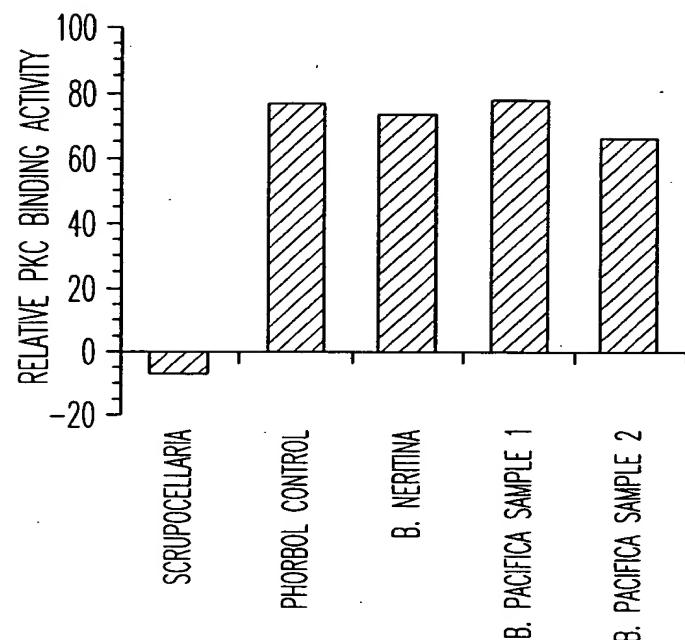


Fig. 21

FIG. 22A

SEQID NO:11	aaattgggtg atccgataga	agtccgagaca	ttggcagaat	cgtttcgagt	ctatacggac	60
100	aagcgtcatt actgtgtct	gggttcgta	aaaagtaata	ttggtcattt	gggggttagt	120
180	gcttggatag	caaaagtattg	ttgtctttgc	aggcatcgcat	gttaccacg	180
240	acgattcatt gtgaggatgt	aaaccacag	atgcgttgg	aaggtagccc	cttttatac	240
300	aatacggaat taaaggcttg	gcagtcttgt	gacggttatc	cacgacgggc	tggtgtcagt	300
360	tcttttgtg tcaagtggcac	caatgcacat	ctgttattag	aagaataatac	tcaaccggata	360
420	acatcaccat tacaaaatac	tattttaccc	cagaacgggt	tgttttattgt	tccactatct	420
480	gcaaaaatg atgaatgttt	aaatgcttgt	gtcgaaacgac	tgtttttttt	tctaaaaaaggc	480
540	aggcaatccg atacatataa	aaaatatcc	tttaagtgtata	cagtccttat	atgttttagat	540
600	ttagcatata ccctccagg	cgttaggaa	gogatgacaa	aaccgagttgc	ctttgttagtg	600
660	aaaacaacaa tagagttaat	ggaaaaattt	aatgcattta	tagaaaaaca	aaatactata	660
720	aaagcaagta atataaaagg	ttgttactac	tcttcgacta	aaacatcgag	tccatttgat	720
736	aatgaatcga	ctgatc				736

FIG. 22B

cgatttagtg atccaaatgg atggcaggca ctctcgaaagg cgtttaggaga gggaaacacaaa 60 SEQID NO:13
cgaaaaacagt ttgcggat cggttcagta aaatcaaata ttggtcatct ggatgttgct 120
gctggagtcg ttggctgtat caagacagca ttgtcgctgc agcacccgtt gttggctccc 180
acgatcaact acggaaagcacc caatcgggaa atcaattttg aacatcacc ctttcatgtg 240
atgtatgaaac tcacgaggatg gcggggatcaa ggtggaccac ttctgtgtgg tgtcagctcg 300
tttggaaatgg gt 312

FIG. 22C

caattggcg accctattga actgcaaggca ctggccgatg tttatagatgt tgatcaaactgg 60 SEQID NO:15
cgccaaaaaca cctgtgccct cggctcggtt aaaaagcaata ttggccatac ctctgcggcc 120
tctgggtgtgg ctggataca caagggtgtgg ttatcgctta agcatcgaca attagtagcg 180
aggcctgcatt ttaataggcgc caatcaccac ttgtatgttc aacagtgcgc tttttatgtc 240
aataccggc taaggcccttg ggatcaaggca gagggactag aagaaggccg ccgcgggct 300
cggttcaggatc tttttgtgtt cagt 324

FIG. 22D

gagttatggag atccaaatggg attgacggct gcaggctggcgt tttttggacgt aggacgaaat 60 SEQID NO:17
cagaaaaatc gttgtgtggt cggatcagta aaaggccaaata ttagtcacct ggaaggcagcc 120
gggggtattt ctggactgtt caaaggcagta ctggcaatgc agcatggcgt gattccacag 180
caattacact gcaaaaggaaacc gaggctctcat atccctggaa aacgtctggc tctcgatgtt 240
gtacaaggaggc agactgtctg gccggaaatgt gaaggaggcgaa tcggggctgt aacaggcgtcg 300
gatttagcgt 308

FIG. 22E

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SEQID NO:19
caacttggcg atgaaataga agttcgcgct cttagtaaag ttcacagttcc 60
ttgtgtctgt aaaaaggcaac ataggctatg ccaacgcagg aacggggcatt 120
ttaaaacggt ttatggttta taccatggca aatgtcacc caatgcaggc 180
tttgaaacctt gacgcgtttc attttgcatt accaaaaact 240
ttgcttacat ggccggagtg ttatgttcga cgggcggcggc 300

FIG. 22F

FIG. 22G

FIG. 22H

ccactcgcg acccaatcga gatggcagca ttaaaacagg ctttggac tcaaaagaaa 60 SEQID NO:25
 aaatactgtg cgatagggtc ggtggaaaggc aaccattggc atgcccatac ggcggctggc 120
 gtcgtggc tcataaggac ggtgatggca ctcaaggccg gtcaagatacc gcctagcttg 180
 cactttgaga cccccaatcc gcagatcgat ttggccgaca gtcctttta tgtaaataaca 240
 accttggaaag attggaaacac caacgggttt ccggccggc cggccgtggc 300
 atcggt 306

FIG. 22I

gtggtcggag atccgattga ggtcggtgg aagacgaaag cctatcaagg gcacactcag 60 SEQID NO:27
 gaacgtcaat actggggact ggttcgggt aagacgaaata ttggccatac ggactcggt 120
 gctggcatgt ctggacttct caagatcgatc atggcgatga agcatcgta actggccggc 180
 agcttggatt ttgaaaacacc aaatccagac ctggatctgg agaatagtcc gttttcatc 240
 cagacgaaagc tgaaggattg gggaaagtgtg gggccctcggtc gtgcgcgtt gagttcggtt 300
 ggtttgggt 309

FIG. 22J

gatggaaactc attaccaccc acaaaaaagt ccgttcttc aacggggtg atttaataaa 60 SEQID NO:29
 ccagctaatt aacgaaacaac aaaaaggca aacgggcaaa ctcatcagg ccttatttgc 120
 ggtggatttgt ttaagttatg atgaactcgg ttatattccca ttcccttaaat ccgggtgggc 180
 gttgtcttc cacctcatca gtaaaacgta tgagaaagcc agtattatca tcagcaccaa 240
 tctggcttt gggaaatgga acagtgtgtt tggtgtgcc aagatgacca ccgcgttatt 300
 ggtatcgatc acgatcatt gttcaatcat gaaagttagt ttccacgggtg ggacagttt agatgcaaac 420
 ggaggtcgg aaacagacat ctttaagtgc aatttggaaaa ccaatgtgtt aatttgtggct aagatcaata 480
 cccgggtcgg aaaaataat tttttatttg attatgtga ttccacgtttaaaa aaaaaatact ataaatatgtaa 540
 aataatattt caacttattt ttgtatggtc gttgttgggg aatttttttgtt gagttatcga 600
 gatattttga aggctttaca ggatgaaaaaa attagtttttg aagaggctaa atataaattttaa 660
 ataaaaaaa aagataaaaaa atccaaacag cgtttaaatc aatgtcgatc attaaatcgaa 720
 tcgatggaaa ttacgccccaa aatagtgaat aattacgggtt tagtattttt gggcggttcat 780
 ttatttggaa aactccgtct gagtgaatgg aaagctgcca acccttaaccctt taatgtaaatgtt 840
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 tatccatcac taaccggctt tggccggcc tttgaaggtat cgggaggtgtat tcgtcaagttg 960
 ggtgaacaca atggggggc atgctgccta tggacgggtt ccacaaggatt acgtggtacg aaaaacccaaag 1080
 gacttatctt ttgaggatgc ctgttagcttc tcacaacgat ccatttggctt ttgcgcacgtt ctatcacagt 1140
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 gacccggagaag acaaggctgc ttggcacttca gtttggggcgtt ttttttttttgc 1260
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 gggcggttttttgc ttttttttttgc ttttttttttgc 1440
 tctctgcgtt ttaatcaatc cgttcaacc ttggggatgc ttttttttttgc 1500
 gatgtatggct ttatcggttca ttttttttttgc 1560
 tttagtgtcaa ccgtgtccgc ttttttttttgc 1620
 tggtgtccgc ttttttttttgc 1680

FIG. 22K

gtctctgaaag ggaggcatat aggttaaagtcc gtttgtgagtc atacaggcac agagcccgatg 1740
 gatttgcaagc agcgctgtat tgacaatgtta ttgaaggcaag gccaatggc ggccttggcc 1800
 gcgacagggg gaaaaaggcg ggtgtgggt ggtactgggt tcaatggacaa accgtctccct 1860
 gctgttggta tagaggaggcg ttatgtggaa gggatagcggt tgatgtgtct gtcaggccag 1920
 tatccgaagt cgaaggacact gggcaattt tggcagacc tggcagacc tagggatgg agtggatgtc 1980
 atctcaggaa ttccctgtga tcgctggtcg ttagaagggtt attactcgcc aataccggaa 2040
 ggggttaaaa cgtatgtaa gtggatgggt tttttggagg acatggatgg ttgtatcccg 2100
 ttgttttttg cgtatctcc tggggaaaggcg gaaggatgg accccacaggca acggatattt 2160
 tttagagaatg cattggatgt tataggaggat ggggggattn accctaagat gttatcccgt 2220
 agtcgatgtg gggatgttggt gggatgttggt gcaaatgtt acaggcgctt aatgaaacagt 2280
 agccactcaa cgagtctcgaa attaatgtaa gaatttagggca acaaacttcc cattttatct 2340
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 ggaacaatag agtcgtttgc tgcaatcat gcaagttacag ttatattcc ttgtgtcagcg 3240
 aaaagtatcata ataggttata cacaatgtt cttttttttt aaaaacgtatg tttttttttt aaaaacgtatg 3300
 caggttactg acgctaaaaa aatcacaata gatcacatgg aatgtcgctt gttggatata 3360

FIG. 22K (cont'd)

gcctatactt tgcaagtggg tcgcaggca atggacaaac ggataagttt tattgtcaac 3420
 acaaaggcaag cactcgtggaa aagcgttaat gctttctag aagaaggaaaa gactataaca 3480
 gactgttacc actattttt tgatagtgtac aaaccgtctaa cagaattttt ccgtttagac 3540
 gaagatgaca aagtattaaat aaacagctgg ataaagtcaaa gtcataatca caaatttagcc 3600
 gaaggcctggaa gccaaggact cgataatcgac tggacgctac tctataccca ctcataacc 3660
 ctcgtcgca ttagccctggcc cactgtatccc cttgcccagg accgtactg gctaccagaa 3720
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 acgttagcga tattgtatcaa cgattgtctta caggcattac cagggtgtt aagtgggtgag 4200
 caattaaataa cggatattat ttcccccaat ggttcgtatgg agaaaatggg aggcttatat 4260
 aaaaataataa ggatttgaga ttattgttaat cagtgtgttg gagacctgtct cgtcccgat 4320
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 cgaaatatac acgaaacgggt cagccatgtg aggccaggcat tggggcccaa cggtttatcg 4680
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 aaggcgtggc aaggcggtact ggaggcggtcg ggttttggat acgtggaaatt tccgtccat 4860
 gacgcgtcgatg agttgggtca acaaattatc ctggcaacca acgcctatgc gaacgttgct 4920
 agcgatcttg cgacatcggt gattgtatcat gcccccaaga gattggccatc cgccgagggtc 4980
 agcatggatg agaggatgtg ccatgtatgccc atgatgaaagg catggtcaa acagttgttg 5040

FIG. 22K (cont'd)

gtagagcaat tatcccagtc tttaaaactg gatcatgaaatg agattcaccc tgacgaaatcc 5100
 ttgcgcatt atgggttga ttccattacc ggtgtctagt ttatccaaca gcttaatgac 5160
 acgctgacac tgactttaaa gacgggtgtt ttgtttgatc acagctcggt aacccgactg 5220
 acggccatc tgtttatctg ctatggat gatatcgcc agtggtagc aacggcacca 5280
 gggttggatg atcatccaca gaggttcgtc agtcagggtt tgccgtaaag gtcggcaggca 5340
 agcacacaag ccaaggccctt gccttcagtc ccccttcgtt tatcgatgg agtcaccgggtt 5400
 caacaggagt cgatagcgat tattggatg agggacgggt ttgggggtc agaaaacactg 5460
 gaaaggcttt gggcaacaggc ggacacagggt ttctctcaagg atatggatca atttgatcc 5520
 gggccacaag cggagactta ctacggcagt ttgtggatg agttatatgg accggcaaca acgtgtttt 5580
 ctctttta atctctccgg tggtggaaagg agttatatgg tgcaacccgc gtcacgttgg 5640
 ctggaggaaat ccttggaaatgc actggaggaaat gcggtttatg tgggtgtatgg catagaaggc 5700
 aaggcggttg gtatttatgc cgggttcgtt tccgggtgact acggacaact gttggggcgcac 5760
 caaccccgcc cccaggcttt ttggggcaat gccaggttcta ttatcccgcc cgggattggcc 5820
 tattattaa atcttcaggg ccctgttacc gcggtggata ctgcgtgttc aagtttctctg 5880
 gtggcggtgc atttggcctg ccaggcccta caccctggatg aaatggagat ggccttggca 5940
 ggagggttgtt ctctttatcc aacccccatc attttatgg tctttggatg gtggcagatat 6000

FIG. 22K (cont'd)

SEQID NO:30
 ancaatttat nacatccncc ggaaaaanacg aacggtcacc atntaggcag gcattggggc 60
 caacggttat ttttttaaat gagtttaacca aaaaagngtt tttnaagtgt aaattgggtt 120
 gncganggtt ggcccttattt aananaggga ttngngtattc ttgaaaccca gggtttatcc 180
 ctaacagtgc aancggtaact gaggcgctcg ntttggttac gtgaatttcc gctccatgac 240
 gctcggtgatc aatcggtcaaca aatcatccctg gcaaccaacg cccatggaa cgttggtagcg 300
 atcttgcac atcggtgatt gatcatggcc ctaaaggaggatt gccatccgg gaggtcagca 360
 tggataaaga gtagccatgatg tgccatgatg aaggcatcg aatggatattc tcaaacagtt gttggttagag 420
 caattatccc agtctttaaa actggatatac aatggatattc accctgacga atcccttgcc 480
 gattatggtg ttgattccat taccgggtct aatggatattc aacagcttaa tgacacgctg 540
 Kraagackkt gtgtttgctt gatcacagact ggccagttgtt tagcaacggc accaggcttg 600
 tatctgttat ctgactatgg tgatgatatc gtcgtttttt gttttttttt 660
 gttgatcatc cacaggtgt cgtcgttcgtt ggtttttttt 720
 caagccaaagc ctttgccctc agtccccct tcgttatcga tgggtttttttt 780
 gagtcgatag cgattattgg tatgaggcgga cgggtttttttt 840
 ttttggcaac agttggcaca ggggtttttt tttttttttt 900
 cttaactacgg cagkttyctc aaggatatgg atcaatttga tcctctttt 960
 tttaatctc cccgggttgg aggcaggat atggaccggc aacaacgttgg ttttctggag 1020
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 tttggatattt atgccgggtt atgtgtccggt gactacggcac aactgtgggg cgaccaaccc 1140
 ccgccccagg ctttttgggg caatggcaggat tcttattattc cggcccccggat tgccatttat 1200
 tttaatctc agggccctgc taccgggtg gatactggcct gctcaaggttc tctgggtggcg 1260
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 tattcacgga gtgatttgctg gcaatgggtat caantaaaaa cggtcgttagt aamttggaaat 1560
 acgggcaccc agtgcmtaaa tscaaagaac gtttggwtac atgatcgctt 1620
 tgdtgyyaac tkaggcatgatc cggacaggccvd tggacacgggc acgrgdytttta 1680

FIG. 22C

ggtgkaccc arttgayrt daaacyttam acccggvggt ttagacactw adacgsaata 1740
 aagaahaatd htgvchate gsgtcggcnc aaaaccaata kkaaagntgg tgggamacyg gsaccatgg 1800
 wggctggtd tgggggctt gtkkgattt gtttcgttcc aatattgact gcaacaccgg 1860
 caaaaactt ccatcgctac attttactca gggcaatccg aatattgact ttgatcgag 1920
 tcctttat gtgaacaccg agtttcgtga ttggtcgggtt ggtggaggag agacccgttg 1980
 tgcgacggtg agccctttg gatttatgtgg taccaatggc catcgagtga tagaagaagg 2040
 gccgcccgtc gtgcgccaac atgaaagaga gcccgggttat ttaagtggc ttatcgccgc 2100
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 gtacaaccag tactgattca ttgttttagt cttttatcg cttttatcg cttttatcg cttttatcg cttttatcg 3960
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 gtcctcgaca gaataccaaag aggtatgtt gtntaaatgtt tcngtnctg tcaattttaga 4560
 ccaggcaca canagnatag agatggatt tctttatnnta ntaaaaacgt tatctgcagt 4620
 attcgannn acagnacagg gtnnttagata atngtccaaa tacttttcc aggttttggg 4680
 taaaangggat tggaaanccaa 4700

FIG. 22L (cont'd)

gcncttncg cggccggc cgtcttagaa ctagtggatc cccgggctg cagtattcgg 60 SEQID NO:31
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 gttgcagtac acgcaattgt tgtaatgtt cggaggatg aaggaaatgg agaggctttt 360
 gcacaaggcag gtttcgagg agattcctgt ggtatccgcg gatactgtca gcgagaataa 420
 aacctcgact attggaaatc ttccaggccg tttagataca ttacccatca ttgagggtca 480
 ggcatcaat atggaaacaa aaaaatgtt gttatgttca tgaaacatgg gataaatacg gagttgattc 600
 acaaattccc gggaaaataa ttgttcaatc ccaatcaattt gggaaaatgtt tgtagggaaat tatctaaaac 660
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 cgtctccctc acctatgtta tatcttttaa aaaggatttga ggtttctttaa ttaaaaaccar 3300
 3360

FIG. 22M (cont'd)

aaaaattact atttgttgg gaatttaaga caagcttakc rrcgaytgy acyykraakc 3420
cwrjkkgggw ttygmamrwy ckkwaksigt dgtgcaacs g ratwtkragg ttgcgggttt 3480
attaraggcm rtggaaggta ctyaatccca tmcaagtgaca aagcaaatgg atctttggat 3540
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gagctgagat aagaagactt aagtgttga gaatgttata ttttggactt aaaaactctg 4560
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mwwyacrssk sawswnkaws tggscwtgay csygcraaks gcryagtgmw tggakagsmw gytgwtgcar 5640
amygawakac ckarnrtcam acrwmtctk sggkttc aaaaagggtt mmaaat 5686
tcgtaytgma

FIG. 22M (cont'd)

FIG. 22N

tttctaaaaa	ttatccaagg	aacttacctt	ttactcgaaat	taccctaaat	ttttttgaaaa	1740
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cgattggata	atgtctgtct	gttaaaatgtt	gatcaagtggc	gatctatatt	atttaaatca	3300
ggctttnaaaa	aatgttaaag	actttgtttt	accttttgaa	aaacttaataa	ttgagcaag	3360

FIG. 22N (cont'd)

FIG. 22N (cont'd)

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 aaaaattttt ctttaaaaatt taaaagataaag aagactatg tggcaact gtcagaatgg 1320
 gaaaaaaaattt ttgagctaga agtttctgtt aatatgtgg aaaaatcaa atatttaat 1380
 gatgcgaata ataccacact gacgcaattt gctgttgcattt tactgttat 1440
 cgccctctcg a ggttaccaggt acccttgcac atggtcaaca gccgttagaga taaaatagaa 1500
 ttgtgaaataa ttgtatggta ttttgcattca actctgcctt atggatttta ggaacctttc 1560
 caaaaggatt ttctcttattc cnggatggta cttttttaa gtatggaaaa aaaaangggaa 1620
 aggccccc naggattttt taaanggggtt tntcnqqqnnntt ttggatattttt taaanggggtt taaanggggtt

FIG. 220

ccctcaanaa aaaaaaaatt tnttccaaaa aaaaaaaggg gcccttaaa ntccccatta 1740
agggaaattt ttaaattttt taatttcccg ggnaaaaattt tttntttaaa ttccggaaattt 1800
aaggccnaan tggaaattaat tggaaaaattt tccannttgg gtttttaaaa agggaaaaaa 1860
ncccannaat ttgggtttcc ttaaaaanaa aaaaaaanaa ggngggggg cgggggggttc 1920
nttnntggg gnaaaaattt aaaaatttaa tttn 1954

FIG. 220 (cont'd)

anccgaaaaa naccnaagg gnnccggcc cntgtcctnc gagtgcatna taaaaancc 60 SEQID NO:34
 agtnataagn ngnnaacaat antcatgccc cgcgccnc gnaagnaacc tnantgggt 120
 naaggctca agggcatcgg tcaaggaacc ttccggcggg ctttcggcggg cttttgtgtt ggcacaggct 180
 cacgtntaaa aggaaaataa atcatgggtt gttttccgt ggcgcgttgc ataaaattt cacgttgc cggccggcg 240
 acgaatgtc tgtatgcgtt gttttccgt ggcgcgttgc ataaaattt cacgttgc tgcgttgc tctggcttct 300
 aatatctggca cagccgaatt ggcgcgttgc gttttccgt ggcgcgttgc aatccaggaca cagcaact 360
 gaataccaga aagaaaatca cttacccctt ctgacatcag aatccaggaca aagggcagaa atttgcgtt 420
 gAACACCTGG TCAATACGCG TTTGGTGG CAGCAATATT GCGTTGAT GACGTTGGC 480
 gttgagatg atacctctgc tgacaaaag gcaatcagc gttgatgcgtt gacgttgtt 540
 gmcmcggkmw cttwmrast twtcscaaw rragkktywt tmawmaagsm cscygskrky 600
 gswwwtggwr ctawccacgm arcessmwwt y gaaamaccks rkcyggntkw csrawawmwa 660
 cmrsmycasc cttggwawm armrwsmtga syywgckcwg aamaakgtw aamaakgtw ccstcrkgc 720
 cgmttwgkjc aawkttwmac cystrwwr ymctmaamatm garrcsttgm ycgraaaccsc 780
 gmtgaaaaan ncqctghntg nnaatgtvrg gctgtntggat gtcgtntggat gtchcaaaagc aatggcasc 840
 agacaangaa agcgtatggat gaactnnnng ctccctttagtgc tccggccggc caktcatgt 900
 ggaatgttcc ccccsgggg tggatctcg caccagtggc gtcgtatgtt antgnaant 960
 tngantaant tnattnatca tttnngcggg gtttgcgttgc ttatggaaaa ttatggggtt taaggcgtt 1020
 cggggcggcg acctcgncgg gtttgcgttgc ttatggaaaa ttatggggtt taaggcgtt 1080
 ccgttcttc tcgtcataac ttatgtttt tatttaaat accctctgaa aagaaggaa 1140
 acgacaggcg ctgaaaggcg gcttttggc ctctgtcgat tcctttctct ttatggggtt taaggcgtt 1200
 cgtggatga acaatggaa tcaacaaaaa gcagaggtta tcgtatgttgc ggggtcaaaac 1260
 atagaatc gcggccgcat aatacgactc actataggaa tcatattttt ggtgttattta 1320
 aaggaggatgc catcaatcat gttggcaaaa ccaatggctt tagtgtgcct aatccggata 1380
 agcaaacagg tgcattatgt gaggcttgc agcgggtca aatagtcctt catcaagtca 1440
 gttatgtaga agggcatggt gcgggaaaggc gtttaggcga cccaaatggaa attacggctc 1500
 tcagcaaaagg attaaacaat gttatgtgcgca aatttaatgt gaaaatgtca gccaatcaat 1560
 cgtgtttat tggctcggtt aaatccaata tagggaaactg tgaatctgc gaggggact 1620
 gccaggattta gcaaaatgtt gcttacaaaatg aaacatggc aatatgtgcc gtccttgcat 1680
 tcaaaaagaac tgaatccaa tattgtattt tcagcaactc cctttgtgtt taaccaagaa 1740

ctgcgcatt ggcagagacc gctgattgtat gaaaaaacag tgccgagagt tgccggtgtc 1800
 ttttcatcg gggcagggtgg ttccaaatng nttacgtgg gattgaagag tatattgcga 1860
 agataccgac aaataaacacc agggaaatcta taaaaccatcg gtctattttt ccatattcg 1920
 cacgaactgc tgaggcagtgg cggcaaatgg ccagtagat gctggcatt attggaaaga 1980
 acaaggaaaga cagcgtggtt acccccttaa tagatattgc ttatcatcg cagtaggac 2040
 gcgaaaggcaat ggtatggaccc ttggggttta ttgtgaggttc aaccggatgc aaccggatgc 2100
 gaactacgaa gatatctca aacacacgt gatatggaaag agctttatcg aggtcagggt 2160
 aatcgatcg aagacaccc tcttactatg gggctggat ggaagatctc tcttggaggt 2220
 atcccacca ttgggatata aaaaacgaaa aactggtctt aagttaatcg ccaattattt 2280
 gggatttaaa agggtttt gtggatttaa wtkggggrkr agwtatassw tkkyttmcca 2340
 aargrkgwtw ktccycsgr matkarmkka ytaccctrcc ytyyggcrs matattttta 2400
 rgwtkktamn swtyrnmcct tcwtwccty ttktgrccctt aggnccaaa ttatattng 2460
 tttnngggaa atttngttt aaaaagaat tcggtaanc ccactnccn ttaaactttc 2520
 atttttgggg gnaatgggtt ttatggnaa cccattccna aaaccaaaa nggcccttt 2580
 ttttccat tcnnaaaaaa accaaaattt ggccctttt ttgggggggg gaaaaaaa 2640
 acccnaangg gggaaaaattn tttttaaaaaa aa 2672

FIG. 22P (cont'd)

nnnnnnttc cnattccctt gggcggaaat ttttgcctt gggncggat aaccaaaggaa 60 SEQID NO:35
 cccttttcn ggcccttaa aaaaacccaa tttnccctt ttaatcccc cgaataaaag 120
 aacccttccc aaaaaagggg naanttgaan tgggggnan cntggaaat cccaaaggccaa 180
 aaaaaggccc aaymtcgccc waraacrkkc cawaatss gawaasmcyy ccagawarwa 240
 ttkwtkrrwa mwrawcyagy wwmiscamatc rgrrggttwta tgrrsssrq wmyawwtraa 300
 aarymytcca wyktkttkss grrtcaatka tgssrkwy tcaaymttgg gactcmcyym 360
 tcmmmwttt gaaaaccmwy attatakktr taagsgggc aaataatcaa tgggtggatat 420
 ggttaamcgg ataaaaaaa gcctcaataa attttnctgc caacaactaa gacagctcta 480
 caataaacat aaaagcaata atgagtcct gtgattattt cccatgaaaaaa aaacaatggc 540
 attttaatag atagatctca tactgaatcg aatattgcca ttataggat atcagggtgt 600
 ttcccgatg caaaaatgt taatgtaaattt tggaaaattt taaaaaatgc tcgtcatagt 660
 gttaaagaaa ttccctataa ccgtcttg gatattgata attactttga tacttcttcg 720
 caaacatg cacaggaata tggtaaaca ggagcattt tagaaaaatat cgatctttt 780
 gatcccgctgt tttttaatat ttctccgtt gaaaggcgattt ganangatgc ttatggatcc aactgaacga 840
 ttttccttc aggaatcctg ggggtatttgc cctgtgaaaaa ggggagactac tttttatgtat gcatcaaaact 900
 ntaagtggaa aacgntntgg ggttcatgc ccactgactc tatccctcct gatancnggc ttgttcatcn 960
 ttccaaagca ggataaaact cgttcatgc tagggcctgc agttcacgtt gatancnggc ttgttcatcn 1020
 cttatttattt gaatttgnnt tagggcctgc acggatgtg tagcctcatt ctttagaaattt gtagtggatgg 1080
 gtctttggca gcaatttgctt acggatgtg tcaactcaac tcccaggcctt ttgatcagt caagtcaact 1140
 cattcaggaa ggtggaaata tcaaaaatgtt gccgttgc tggcttsdat caacgtgcaa acggaacgg 1200
 tggtttgttgc tcaaaaatgtt cgattatttt aaaaacccatca aacaaaggaa ttgacgtgg 1260
 attaggggag gcggatascat ttaagggtt gggaaatgtt aacatggaa aacatggaa 1320
 ttagtcaaggc tcaaggatataa agtccacaat tcakttggaa acggatgttt atcaaaaatt 1380
 tmttactgtt ctttagtgc ttackatgtt tsmagccat ggaactggaa ctaaactasg 1440
 tatgatwaat cctgaaacata ttackatgtt agtccatgc tttcas aaataatacty aaaaacackg 1500
 agatccatt gaggytcagg cattamcaga agtccatgc ttraaaaarwa aatattggac atacntttt cccgctgtgt 1560
 gttttgtgca ctagngttct graktkctca gatgttaatm aagggttaatm ttgtccattt cwcancattt acmargwttc 1620
 1680

FIG. 22Q

Ytycrtart twwtaattyw maarstatna mttwttcaww attctatyg tnaawwaccc 1740
ywatttkkw ktaaaamcag cycatwwttw wyyssskgtm attwnyycc ncttwtrw 1800
wmcccmmyt gcgrrcsqtt ttttcgtkk ktgttcrwc akagaatctm mmsyccctt 1860
tygcmmma amrnnttaa acmmtwrc tttttrgr kggsgycccc cnccngggg 1920
gaancccc antgggtccc cnntttggg gggggggnt tngmaangn aaaattttt 1980
tttcatgccc nnanaaaagg tccttccgca accttttta aaaaataaanc ccntcccna 2040
aaaantggg nattggan tgggaattaa aaaggccct tttttacccc cccngtta 2100
atttaatc cccctttt tggtccggg cc 2132

FIG. 22Q (cont'd)

ttaccggctt aacarsyttc catggaaagg taggnttaw atagsccrca tattggccy 1800
 tkggtrgtgg aatrawrgtw atkcskgggg wccwgstamw wagggttggg ttytcääaac 1860
 cawawraamm skgtttytg rrkwwtttt tssmmmmgcc scnaatng aacccccnn 1920
 nrgntaaanc cccnngaaat tnnnttttt ttttnccccc gnncccaan cnaagaaang 1980
 aacctttncg ngttttggg caattaaatt taatttagggc aaaccccccnn ttaatngaa 2040
 gggggncca ntgggnngt tttttngga aaaaaggaaagg gnaatttggg gnaaaaagg 2100
 ccccccääa ntnggttt aaaaaggggg aaaaaaaatn aaccgtttaa aaaaattnnc 2160
 ccccaant 2169

FIG. 22R (cont'd)

FIG. 22S (cont'd)

tagagccgg tatgttggat gaggtaaaac cttttacaga tttaggttg gactcgataa 3540
 atggaggcac ctggatacga aaaatcaata gtcaactatgg attatctatgg actgcgcacga 3600
 aagtatatga ttacccaaat attatttggat tggcaggatg tttaagaaaa caaattattt 3660
 cgaatgtga aaaggcagcat caaccatcta tatcaacaat atttccact tcattggatg 3720
 aattatttggaa aaaaatacaa gaaggtaactt tagggatgaa agaaggccgac caattaattg 3780
 atgaactacc tgattaccat ctagatgg aactccatga gttgttataa gggaaaggcga 3840
 ggtattttg tgcacacccg atggatggta aaaccatttt ggctgaaaag aatttagctc 3900
 aaatcgggc agctttggcg atttggatgg atttgacttg ttatggatgaa ctcaactatg 3960
 ctgtacgc attcccttac ataaatggatgg gaaaatggaa aacaattatgt gtaaaccataat 4020
 tttagagacaa ttgaaaagt ttgttagaac aaggcgttag cacgcgttag ccaattaaag 4080
 taacggcag aggcaatgg gctttcgatc tgataaagtgc atttgatgc acaaattgca gattcgcttg 4140
 aggaaaaggct ttatattt cagaatatgtg ttatgtgca acaaaattgca gaaatcactg 4200
 gtacggcatac tcagggcaag ggatacaacaa cAACGGATAA tgagttgaat gaaatcactg 4260
 gtgcattgaaag gccatacccg ggaaaaactgg gaaaaggctt tgatcgatc tgatcgatc 4320
 cacaaggcgat tatgcaaaactt actcaaaaatgatgttcaact cggaaatgtt aacccggaa 4380
 tttaggttaaac ctggccgcgtaaactc ttatctggat tatgtctcg ggcatttcg 4440
 caaaagacc gactgatata tcgctttatc ttgcgtatcg gtggtcacta cgatcaacat 4500
 tttagttgcca taacggccata acaaggaaaa atatgaaaggc cagggaaatc ttttcccttg 4560
 tggttacgt tgttataagg ttgtttatc atttagactc cctctgttt tactgcaytg 4620
 tggttagcc agtcccgatcc acgtttttg kgggcsrwtt tcaatgtgtct ttttatacac 4680
 tttagatgtcc gaaaakgraa mccamccmcc attgtatatt tytttaact caatggataa 4740
 atgtttata gctaactgtg aaggcttcgt tgccctgttg aactcacgt cattttctc 4800
 tgattttca taaaaggcgt tagtgaaaaa tgaagctggt tctgattttt tatgtacagg 4860
 tttagttcgt aatctaattt aaactttcat atttgatat gcttgcttg atttatcaat 4920
 ttctttccca gtaataattc gtgtgcaaac tagccattta gaaataatc ctaattttatc 4980
 taagtgcata acaaccgtat ttgtcagaca aaatgacgag cagaaaaatc wtctgcctc 5040
 tattctaaa tacwtaggg acaattwtcm cacaaaatgt cactgaggct 5100
 atttcttctyt tgkaatctt atccctaata ttcccagc tttagtgcacca ataaatttata 5160
 tcatawmagt actctgtaaag ccgataatac cttttgttta tatcccaata attggacca 5220

ckgraagmsk wwmckaaws srwgctgtc gtaggggg gctatattgc tggtaggtt 7020
 gcaggattt ttcaagggtt ggttagtgc attcattt tgatcagg tgatttattt 7080
 ctaaggat ttgatcgaga tttactgcca tttactgcca gtaggttct gctattgaaa agcaatggta tggtagcccta 7140
 gtaaatttac atttaatcg cagtgttct gctattgaaa ctattatgta tgccacagg 7200
 tttagtggat taactgtgg ctcaaccttg gaagtggata ctattatgta tgccacagg 7260
 yggaaaccar rmmyyaggg wyytgktyt ksawwrkrs c gctgtmaas krrkyaaaw 7320
 gggaaaggctt tycaaagtnta actgakaayt tttcaaanca agcagaaggc wbtytawttt 7380
 aygcaaggtaa aatagaccgg tatgncaatk aacvccaatg tgstctsgc 7440
 tgaarggtat ggmctaagg mcagcttta tattagtgc tmcaagtggat taataanggt 7500
 agattatggg tttsgttgc cmagaaccgg ttttnttgc caamcccaan tatggccacc 7560
 gtaggtata gtgaagaggc ggcgaagrgm wragttgtat acgggbctg tttadaaatr 7620
 gattttaaa ccagatgaag ncatacgctg agtgnctct tngatngagc ggacttttg 7680
 tgaagtnwat tagtaganc aaaaacnmcaq ataragtcg agtgttcat atggtaggcg 7740
 ctcragcgg gagaatctt gntattgcca taaaggcagg agccacaaa gcagactttg 7800
 atagcaccat agtattcac cctacgggtt ccgaaggagt tgtgactatg agagagccctg 7860
 cgtatattt atagcaatag gccaaggca gctacttgtt ttagtaaggc tattttaca 7920
 aatagtagca tcagataata taktgccgtt gtttacgtt yamtgaatca kcagtkgtma 7980
 wakkagtc ataggcaygms gwrtkatasg kgkattcata yyrtcawaa syaaykckgt 8040
 cgtcggggg yataatkctc akrataataat wcrttcgasw cctgtysakk cccwaccacr 8100
 satacywssc aaagarttgy agratcrag ckwtgsakws tgamcgntgs matnakgttc 8160
 aacgcatgkccagccctkat agcatcygac caytsaggc caawrkgmgt taayccagt 8220
 gtwcngtts atrnrsgacs mgktaatggt mgttgwtst wrkawgccsg mtcttmmaaa 8280
 mcmnsannmr acgtacaagm rtgwcacmg krgcytrya snmattmgct atcamrcnca 8340
 yssrrggkk ggycttmaawa arargggcaa aaaaaaaaaan 8380

FIG. 22S (cont'd)

Lys Leu Gly Asp Pro Ile Glu Val Glu Thr Leu Ala Glu Ser Phe Arg SEQIDNO:11
1 5 10 15

Val Tyr Thr Asp Lys Arg His Tyr Cys Ala Leu Gly Ser Val Lys Ser
20 25 30

Asn Ile Gly His Leu Gly Val Gly Ala Gly Ile Ala Gly Val Thr Lys
35 40 45

Val Leu Leu Ser Leu Gln His Arg Met Leu Pro Pro Thr Ile His Cys
50 55 60

Glu Asp Val Asn Pro Gln Ile Ala Leu Gln Gly Ser Pro Phe Tyr Ile
65 70 75 80

Asn Thr Glu Leu Lys Pro Trp Gln Ser Gly Asp Gly Ile Pro Arg Arg
85 90 95

Ala Gly Val Ser Ser Phe Gly Val Ser
100 105

Lys Leu Gly Asp Pro Ile Glu Val Glu Thr Leu Ala Glu Ser Phe Arg SEQID NO:12
1 5
Val Tyr Thr Asp Lys Arg His Tyr Cys Ala Leu Gly Ser Val Lys Ser
20 25 30
Asn Ile Gly His Leu Gly Val Gly Ile Ala Gly Val Thr Lys
35 40 45
Val Leu Ser Leu Gln His Arg Met Leu Pro Pro Thr Ile His Cys
50 55 60
Glu Asp Val Asn Pro Gln Ile Ala Leu Glu Gly Ser Pro Phe Tyr Ile
65 70 75 80
Asn Thr Glu Leu Lys Pro Trip Gln Ser Gly Asp Gly Ile Pro Arg Arg
85 90 95
Ala Gly Val Ser Ser Phe Gly Val Ser Gly Thr Asn Ala His Leu Val
100 105 110
Leu Glu Glu Tyr Thr His Arg Val Thr Ser Pro Leu Gln Asn Thr Ile
115 120 125
Leu Pro Gln Asn Gly Leu Phe Ile Val Pro Leu Ser Ala Lys Asn Asp
130 135 140

Glu	Cys	Leu	Asn	Ala	Cys	Val	Glu	Arg	Leu	Phe	Phe	Leu	Lys	Ser		
145																
													155	160		
Arg	Gln	Ser	Asp	Thr	Tyr	Lys	Lys	Tyr	Ser	Leu	Ser	Asp	Thr	Ala	Pro	
													170	175		
Ile	Leu	Leu	Asp	Leu	Ala	Tyr	Thr	Leu	Gln	Val	Ser	Arg	Glu	Ala	Met	
													185	190		
Thr	Lys	Arg	Val	Ala	Phe	Val	Val	Lys	Thr	Thr	Ile	Glu	Leu	Met	Glu	
													195	200	205	
Lys	Leu	Asn	Ala	Phe	Ile	Glu	Lys	Gln	Asn	Thr	Ile	Lys	Ala	Ser	Asn	
													210	215	220	
Ile	Lys	Gly	Cys	Tyr	Tyr	Ser	Ser	Thr	Lys	Thr	Ser	Ser	Pro	Phe	Asp	
													225	230	235	240
Asn	Glu	Ser	Thr	Asp												
													245			

FIG. 22U (cont'd)

Arg Leu Gly Asp Pro Ile Glu Leu Ala Ala Leu Ser Lys Ala Phe Glu SEQID NO:14
1 5 10 15

Glu Gly Thr Gln Arg Lys Gln Phe Cys Gly Ile Gly Ser Val Lys Ser
20 25 30

Asn Ile GLY His Leu Asp Val Ala Ala Gly Val Val Gly Leu Ile Lys
35 40 45

Thr Ala Leu Ser Leu Gln His Arg Leu Leu Pro Pro Thr Ile Asn Tyr
50 55 60

Glu Ala Pro Asn Arg Glu Ile Asn Phe Glu Gln Ser Pro Phe His Val
65 70 75 80 85

Ile Asp Glu Leu Thr Glu Trp Arg Gly Gln Gly Pro Leu Arg Ala
90 95

Gly Val Ser Ser Phe Gly Ile Gly
100

Gln Leu Gly Asp Pro Ile Glu Leu Gln Ala Leu Ala Asp Val Tyr Arg SEQID NO:16
1 5 10 15

Val Asp Asn Trp Arg Lys Asn Thr Cys Ala Leu Gly Ser Val Lys Ser
20 25 30

Asn Ile Gly His Thr Ser Ala Ala Ser Gly Val Ala Gly Ile His Lys
35 40 45

Val Leu Ser Leu Lys His Arg Gln Leu Val Ala Ser Leu His Phe
50 55 60

Asn Ser Ala Asn His His Phe Asp Phe Gln Gln Ser Pro Phe Tyr Val
65 70 75 80 85

Asn Thr Gln Leu Arg Pro Trp Asp Gln Ala Glu Gly Leu Glu Ser
90 95

Arg Arg Arg Ala Ala Val Ser Ser Phe Gly Val Ser
100 105

Glu Tyr Gly Asp Pro Met Glu Leu Thr Ala Ala Ala Ala Val Phe Gly SEQID NO:18
1 5 10 15

Arg Gly Arg Asn Gln Lys Asn Arg Leu Leu Val Gly Ser Val Lys Ala
20 25 30

Asn Ile Ser His Leu Glu Ala Ala Gly Gly Ile Ser Gly Leu Ile Lys
35 40 45

Ala Val Leu Ala Met Gln His Gly Val Ile Pro Gln Gln Leu His Cys
50 55 60

Lys Glu Pro Ser Pro His Ile Pro Trp Lys Arg Leu Pro Leu Asp Leu
65 70 75 80

Val Gln Glu Gln Thr Val Trp Pro Glu Ser Glu Glu Arg Ile Ala Ala
85 90 95

Val Thr Ala Ser Asp
100

Gln Leu Gly Asp Glu Ile Glu Val Arg Ala Leu Ser Lys Val Tyr Gly SEQID NO:20
1 5 10 15

Asp Ser Gln Ser Thr Thr Tyr Leu Gly Ala Val Lys Ser Asn Ile Gly
20 25 30

His Ala Asn Ala Gly Ala Gly Ile Ala Gly Phe Ile Lys Thr Val Leu
35 40 45

Ser Leu Tyr His Gly Lys Ile Ala Pro Asn Ala Gly Asn Thr Glu Pro
50 55 60

Asn Ala Ala Leu Asn Leu Asp Ala Phe His Phe Ala Leu Pro Lys Thr
65 70 75 80 85

Leu Leu Thr Trp Pro Glu Cys Asp Val Arg Arg Ala Ala Ile Ser Ser
90 95

Leu Gly Phe Gly
100

Ala Leu Gly Asp Pro Ile Glu Phe Gly Ala Ile Lys Ala Val Tyr Gly SEQID NO:22
1 5 10 15

Pro Gly Arg Ser Ser Pro Leu Val Leu Gly Ala Ala Lys Ser Asn Ile
20 25 30

Gly His Leu Glu Ala Thr Ala Gly Val Ala Ala Leu Ile Lys Ala Val
35 40 45

Leu Val Leu Gln His Gly Val Ala Pro Ala Asn Leu His Cys His Lys
50 55 60

Leu Asn Pro Leu Leu Asp Ile Asp Gly Phe Asn Val Val Phe Pro Gln
65 70 75 80

Ser Glu Thr Pro Leu His Ser Ser Leu Gln Leu Leu Gly Gly Tyr Gln
85 90 95

Phe Val Arg Val Trp
100

Thr Trp Xaa Ser Leu Leu Arg Trp Gly Leu Leu Gln Asn His Phe Asp SEQID NO:24
1 5 10 15
Pro Tyr Thr Glu Lys Lys Asn Tyr Cys Ala Ser Gly Ser Val Lys Ser
20 25 30
Asn Ile Gly His Leu Thr Ala Ala Gly Val Ser Gly Val Val Lys Val
35 40 45
Leu Leu Ala Leu Lys His Lys Gln Leu Pro Pro Ser Cys His Leu Val
50 55 60
Lys Ile Asn Glu His Ile Asn Leu Glu Asp Ser Pro Phe Tyr Ile Asn
65 70 75 80
Thr Ala Leu Lys Lys Trp Glu Val Ser Glu Gly Glu Ala Arg Arg Ala
85 90 95
Ala Val Ser Ser Phe Gly Ser
100

Pro Leu Gly Asp Pro Ile Glu Met Ala Ala Leu Lys Gln Ala Phe Gly ~~SEQIDNO:24~~
1 5 10 15

Thr Gln Lys Lys Tyr Cys Ala Ile Gly Ser Val Lys Ser Asn Ile
20 25 30

Gly His Ala Asp Thr Ala Ala Gly Val Ala Gly Leu Ile Lys Thr Val
35 40 45

Met Ala Leu Lys Ala Arg Gln Ile Pro Pro ~~Set~~ Leu His Phe Glu Thr
50 55 60

Pro Asn Pro Gln Ile Asp Phe Ala Asp Ser Pro Phe Tyr Val Asn Thr
65 70 75 80

Thr Leu Lys Asp ~~Trp~~ Asn Thr Asn Gly Val Pro Arg Arg Ala Gly Val
85 90 95

Ser Ser Phe Gly Ile Gly
100

FIG. 22B

Val Val Gly Asp Pro Ile Glu Val Val Gly Leu Thr Lys Ala Tyr Gln SEQID NO:28
1 5 10 15

Ala His Thr Gln Glu Arg Gln Tyr Cys Gly Leu Gly Ser Val Lys Thr
20 25 30

Asn Ile Gly His Thr Asp Ser Ala Ala Gly Ile Ala Gly Leu Leu Lys
35 40 45

Ile Val Met Ala Met Lys His Arg Gln Leu Pro Pro Ser Leu Asn Phe
50 55 60

Glu Thr Pro Asn Pro Asp Leu Asp Leu Glu Asn Ser Pro Phe Phe Ile
65 70 75 80

Gln Thr Lys Leu Lys Asp Trp Glu Ser Val Gly Pro Arg Arg Ala Ala
85 90 95

Leu Ser Ser Phe Gly Leu Gly
100

Met Val Val Val Glu Glu Phe Phe Val Ser Tyr Arg Asp Ile Leu Lys SEQID NO:38
1 5 10 15

Ala Leu Gln Asp Glu Lys Ile Ser Phe Glu Glu Ala Lys Tyr Lys Leu
20 25 30

Ile Lys Arg Lys Asp Lys Lys Ser Lys Gln Arg Leu Asn His Asp Arg
35 40 45

Glu Leu Asn Arg Ser Met Asn Ile Thr Pro Lys Ile Val Asn Asn Tyr
50 55 60

Gly Leu Val Leu Gly Gly His Leu Phe Glu Glu Leu Arg Leu Ser
65 70 75 80

Glu Trp Lys Ala Ala Asn Pro Asn Pro Asn Glu Val Ser Ile Gln Val
85 90 95

Lys Ala Ser Ala Ile Ser Phe Thr Asp Thr Leu Cys Val Gln Gly Leu
100 105 110

Tyr Pro Ser His Tyr Pro Phe Val Pro Gly Phe Glu Val Ser Gly Val
115 120 125

Ile Arg Gln Val Gly Glu His Ile Thr Asp Leu His Val Gly Asp Glu
130 135 140

Val	Ile	Ala	Phe	Thr	Gly	Ser	Ser	Met	Gly	Gly	His	Ala	Ala	Tyr	Val
145									155						160
Thr	Val	Pro	Gln	Asp	Tyr	Val	Val	Arg	Lys	Pro	Lys	Asp	Leu	Ser	Phe
	165								170						175
Glu	Asp	Ala	Cys	Ser	Phe	Pro	Leu	Ala	Phe	Ala	Thr	Val	Tyr	His	Ser
	180								185						190
Phe	Ala	Arg	Gly	Lys	Leu	Ser	His	Asn	Asp	His	Ile	Leu	Ile	Gln	Thr
	195								200						205
Ala	Thr	Gly	Gly	Cys	Gly	Leu	Met	Ala	Leu	Gln	Leu	Ala	Arg	Leu	Lys
	210								215						220
Gln	Cys	Val	Cys	Tyr	Gly	Thr	Ser	Ser	Arg	Glu	Asp	Lys	Leu	Ala	Leu
	225								230						235
Leu	Lys	Gln	Trp	Ala	Leu	Pro	Tyr	Val	Phe	Asn	Tyr	Lys	Thr	Cys	Asn
									245						240
Ile	Asp	Glu	Glu	Ile	Gln	Arg	Val	Ser	Gly	His	Arg	Gly	Vall	Asp	Val
	260								265						270
Val	Leu	Asn	Met	Leu	Pro	Gly	Glu	His	Ile	Gln	Gly	Leu	Asn	Ser	
	275								280						285

FIG. 2200 (cont'd)

Leu Ala Lys Gly Gly Arg Tyr Leu Glu Leu Ser Met His Gly Leu Leu
290 295 300

Thr Asn Glu Pro Val Ser Leu Ser Ser Leu Arg Phe Asn Gln Ser Val
305 310 315 320

Gln Thr Ile Asn Leu Leu Gly Leu Leu Asn Lys Gly Asp Asp Gly Phe
325 330 335 340

Ile Gly Ser Val Leu Ala Gln Met Val Ser Trp Ile Glu Ser Gly Asp
345 350 355 360

Leu Val Ser Thr Val Ser Arg Ile Tyr Pro Leu Asp Gln Ile Gly Glu
365 370 375 380

Ala Leu Arg Tyr Val Ser Glu Gly Glu His Ile Gly Lys Val Val Val
385 390 395 400

Ser His Thr Ala Thr Glu Pro Met Asp Cys Arg Gln Arg Cys Ile Asp
405 410 415 420

Asn Val Leu Lys Gln Gly Gln Met Ala Ala Leu Thr Ala Thr Gly Gly
425 430

Ala Val Gly Ile Glu Glu Arg	Leu Leu Glu Gly Ile Ala Val Ile Gly	
435	440	445
Leu Ser Gly Gln Tyr Pro Lys	Ser Lys Thr Leu Glu Gln Phe Trp Gln	
450	455	460
Thr Leu Ala Asp Gly Val Asp	Cys Ile Ser Glu Ile Pro Ala Asp Arg	
465	470	475
Trp Ser Leu Glu Glu Tyr Tyr	Ser Pro Ile Pro Glu Gly Lys Thr	
485	490	495
Tyr Cys Lys Trp Met Gly Val	Leu Glu Asp Met Asp Cys Phe Asp Pro	
500	505	510
Leu Phe Ala Ile Ser Pro Arg	Glu Ala Glu Val Met Asp Pro Gln	
515	520	525
Gln Arg Leu Phe Leu Glu Asn	Ala Trp Ser Cys Ile Glu Asp Ala Gly	
530	535	540
Ile Asn Pro Lys Met Leu Ser	Arg Ser Arg Cys Gly Val Phe Val Gly	
545	550	555
Cys Gly Ala Asn Asp Tyr Ser	Ala Leu Met Asn Ser Ser His Ser Thr	
565	570	575

FIG. 22DD (cont'd)

Ser	Leu	Glu	Leu	Met	Lys	Glu	Leu	Gly	Asn	Asn	Ser	Ser	Ile	Leu	Ser
	580														
Ala	Arg	Ile	Ser	Tyr	Phe	Leu	Asn	Leu	Lys	Gly	Pro	Cys	Leu	Ala	Ile
	595														
Asp	Thr	Ala	Cys	Ser	Ser	Ser	Leu	Val	Ala	Ile	Ala	Glu	Ser	Cys	Asn
	610														
Ser	Leu	Val	Leu	Gly	Thr	Ser	Asp	Leu	Ala	Ile	Ala	Gly	Gly	Val	Leu
	625														
Leu	Met	Pro	Gly	Pro	Ser	Leu	His	Ile	Gly	Leu	Ser	His	Gly	Glu	Met
	645														
Leu	Ser	Val	Asp	Gly	Arg	Cys	Phe	Thr	Phe	Asp	Gln	Arg	Ala	Asn	Gly
	660														
Phe	Val	Pro	Gly	Glu	Gly	Val	Gly	Val	Val	Leu	Lys	Arg	Met	Ser	
	675														
Asp	Ala	Val	Arg	Asp	Gly	Asp	Pro	Ile	Arg	Ala	Val	Ile	Arg	Gly	Trp
	690														
Gly	Val	Asn	Gln	Asp	Gly	Arg	Ser	Asn	Gly	Ile	Thr	Ala	Pro	Ser	Ser
	705														

FIG. 22DD (cont'd)

Lys Ala Gln Ser Ala Leu Glu Gln Glu Val Tyr Gln Arg Phe Asn Ile
725 730 735

Asp Pro Ser Ser Ile Thr Leu Val Glu Ala His Gly Thr Gly Thr Lys
740 745 750

Leu Gly Asp Pro Ile Glu Val Glu Ala Leu Ala Glu Ser Phe Arg Val
755 760 765

Tyr Thr Asp Lys Arg His Tyr Cys Ala Leu Gly Ser Val Lys Ser Asn
770 775 780

Ile Gly His Leu Gly Val Gly Ala Gly Ile Ala Gly Val Thr Lys Val
785 790 795 800

Leu Leu Ser Leu Gln His Arg Met Leu Pro Pro Thr Ile His Cys Glu
805 810 815 820

Asp Val Asn Pro Gln Ile Ala Leu Glu Gly Ser Pro Phe Tyr Ile Asn
825 830 835 840

Thr Glu Leu Lys Pro Trp Gln Ser Gly Asp Ser Ile Pro Arg Arg Ala
845 850 855 860

Gly Val Ser Ser Phe Gly Phe Ser Gly Thr Asn Ala His Leu Val Leu

FIG. 22DD (cont'd)

Glu	Glu	Tyr	Leu	Pro	His	Ser	Thr	Gly	Thr	Ile	Glu	Ser	Phe	Ala	Ala
865															
														875	880
Asn	His	Ala	Ser	Thr	Val	Ile	Ile	Pro	Leu	Ser	Ala	Lys	Ser	His	Asn
														885	895
Ser	Leu	Tyr	Thr	Tyr	Ala	Gln	Thr	Leu	Leu	Ile	Phe	Leu	Lys	Arg	Ser
														900	910
Gln	Val	Thr	Asp	Ala	Lys	Lys	Ile	Thr	Ile	Asp	His	Met	Glu	Cys	Arg
														915	925
Leu	Leu	Asp	Leu	Ala	Tyr	Thr	Leu	Gln	Val	Gly	Arg	Glu	Ala	Met	Asp
														930	940
Lys	Arg	Ile	Ser	Phe	Ile	Val	Asn	Thr	Lys	Gln	Ala	Leu	Val	Glu	Lys
														945	955
Leu	Asn	Ala	Phe	Leu	Glu	Lys	Glu	Lys	Thr	Ile	Thr	Asp	Cys	Tyr	His
														955	960
Tyr	Leu	Phe	Asp	Ser	Asp	Lys	Pro	Ser	Thr	Glu	Ile	Phe	Arg	Leu	Asp
														965	975
Glu	Asp	Asp	Lys	Val	Leu	Ile	Asn	Ser	Trp	Ile	Ser	Gln	Ser	Gln	Tyr
														995	1000

FIG. 2200 (cont'd)

His Lys Leu Ala Glu Ala Trp Ser Gln Gly Leu Asp Ile Asp Trp Thr	
1010	1015
Leu Leu Tyr Thr His Ser Ser Thr Pro Arg Arg Ile Ser Leu Pro Thr	
1025	1030
Tyr Pro Phe Ala Arg Asp Arg Tyr Trp Leu Pro Glu Lys Pro Arg Tyr	
1045	1050
Asn Ala Ala Asn His Pro Val Ser Asn His Gln Thr Thr Gln Asn	
1060	1065
His Ser Arg Phe Ala Ile Asp Thr Asp His Asp Val Val Ala Glu Ile	
1075	1080
Met Gln Lys Thr His Gln Gln Glu Leu Glu Gln Trp Leu Leu Lys Leu	
1090	1095
Leu Phe Val Gln Leu Gln His Met Gln Ile Phe Gln His Arg Val Phe	
1105	1110
Glu Thr Ala Thr Ala Leu Arg Gln Ser Ala Gly Ile Val Asp Lys Tyr	
1125	1130
Asp Arg Trp Trp His Glu Cys Leu Ser Val Leu Gln Asp Ala Gly Tyr	
1140	1145
1150	

FIG. 22DD (cont'd)

Leu Glu Trp Lys Asp Asp Ser Val Ala Ala Gln Ala Leu Glu Ser
1155 1160
Glu Ser Gln Glu Ala Trp Trp Ser Arg Trp Asn Thr Glu Tyr Lys His
1170 1175
Tyr Gln Asn Asp Pro Glu Lys Lys Thr Leu Ala Ile Leu Ile Asn Asp
1185 1190 1195 1200
Cys Leu Gln Ala Leu Pro Gly Val Leu Ser Gly Glu Gln Leu Ile Thr
1205 1210 1215
Asp Ile Phe Pro Asn Gly Ser Met Glu Lys Met Glu Gly Leu Tyr
1220 1225 1230
Lys Asn Asn Arg Ile Ala Asp Tyr Cys Asn Gln Cys Val Gly Asp Leu
1235 1240 1245
Leu Val Gln Phe Ile Glu Ala Arg Leu Ser Arg Asp Ala Asn Ala Arg
1250 1255 1260
Ile Arg Ile Ile Glu Ile Gly Ala Gly Thr Gly Gly Thr Thr Ala Ile
1265 1270 1275 1280
Val Leu Pro Met Leu Gln Ala Tyr Gln Asp His Ile Asp Thr Tyr Tyr Cys
1285 1290 1295

Tyr Thr Asp Val Ser Lys Ala Phe Leu Met His Gly Gln Glu His Tyr
 1300 1305
 Gly Glu Gln Tyr Pro Tyr Leu Ser Tyr Cys Leu Cys Asn Ile Glu Gln
 1315 1320 1325
 Asp Leu Val Ala Gln Gly Ile Ser Val Gly Asp Tyr Asp Ile Ala Ile
 1330 1335 1340
 Ala Ala Asn Val Leu His Ala Thr Arg Asn Ile His Glu Thr Val Ser
 1345 1350 1355 1360
 His Val Arg Gln Ala Leu Ala Ala Asn Gly Leu Leu Ile Leu Asn Glu
 1365 1370 1375
 Phe Ser Gln Lys Ser Val Phe Ser Ser Val Ile Phe Gly Leu Ile Asp
 1380 1385 1390 1395
 Gly Trp Ala Leu Ser Glu Asp Thr Gly Ile Arg Ile Pro Gly Ser Pro
 1395 1400 1405
 Gly Leu Tyr Pro Lys Gln Trp Gln Ala Val Leu Glu Ala Ser Gly Phe
 1410 1415 1420 1425
 Gly Asp Val Glu Phe Pro Leu His Asp Ala Arg Glu Leu Gly Gln Gln
 1430 1435 1440

FIG. 22DD (cont'd)

Ile Ile Leu Ala Thr Asn Ala His Ala Asn Val Ala Ser Asp Leu Ala
1445 1450 1455
Thr Ser Val Ile Asp His Ala Pro Lys Arg Leu Pro Ser Ala Glu Val
1460 1465 1470 1475
Ser Met Asp Glu Arg Val Ser His Asp Ala Met Met Lys Ala Ser Val
1480 1485
Lys Gln Leu Leu Val Glu Gln Leu Ser Gln Ser Leu Lys Leu Asp Met
1490 1495 1500
Asn Glu Ile His Pro Asp Glu Ser Phe Ala Asp Tyr Gly Val Asp Ser
1505 1510 1515 1520
Ile Thr Gly Ala Ser Phe Ile Gln Gln Leu Asn Asp Thr Leu Thr Leu
1525 1530 1535
Thr Leu Lys Thr Val Cys Leu Phe Asp His Ser Ser Val Asn Arg Leu
1540 1545 1550 1555
Thr Ala Tyr Leu Leu Ser Asp Tyr Gly Asp Asp Ile Ala Gln Trp Leu
1555 1560 1565 1570 1575
Ala Thr Ala Pro Ala Leu Val Asp His Pro Gln Ser Val Val Ser Gln
1570 1575 1580

Val	Leu	Pro	Glu	Arg	Ser	Pro	Ala	Ser	Thr	Gln	Ala	Lys	Pro	Leu	Pro
1585		1590													1600
Ser	Val	Pro	Pro	Ser	Leu	Ser	Met	Glu	Ser	Pro	Val	Gln	Glu	Ser	
	1605						1610								1615
Ile	Ala	Ile	Ile	Gly	Met	Ser	Gly	Arg	Phe	Ala	Ala	Ser	Glu	Asn	Leu
		1620					1625								
Glu	Ala	Phe	Trp	Gln	Gln	Leu	Ala	Gln	Gly	Val	Asp	Leu	Val	Glu	Pro
		1635					1640								1645
Ala	Ser	Arg	Trp	Gly	Pro	Gln	Ala	Glu	Thr	Tyr	Tyr	Gly	Ser	Phe	Leu
			1650				1655								1660
Lys	Asp	Met	Asp	Gln	Phe	Asp	Pro	Leu	Phe	Asn	Leu	Ser	Gly	Val	
			1665				1670								1675
Glu	Ala	Ser	Tyr	Met	Asp	Pro	Gln	Arg	Cys	Phe	Leu	Glu	Ser		
			1685					1690							1695
Trp	Asn	Ala	Leu	Glu	Asn	Ala	Gly	Tyr	Val	Gly	Asp	Gly	Ile	Glu	Gly
			1700					1705							1710
Lys	Arg	Cys	Gly	Ile	Tyr	Ala	Gly	Cys	Val	Ser	Gly	Asp	Tyr	Ala	Gln
			1715					1720							1725

FIG. 22 DD (cont'd)

Leu Leu Gly Asp Gln Pro Pro Gln Ala Phe Trp Gly Asn Ala Ser
1730
1735

Ser Ile Ile Pro Ala Arg Ile Ala Tyr Tyr Leu Asn Leu Gln Gly Pro
1745 1750 1755 1760

Ala Thr Ala Val Asp Thr Ala Cys Ser Ser Ser Leu Val Ala Val His
1765 1770 1775

Leu Ala Cys Gln Ala Leu His Leu Asp Glu Met Glu Met Ala Leu Ala
1780 1785 1790

Gly Gly Val Ser Leu Tyr Pro Thr Pro Ile Val Glx Val Phe Ala
1795 1800 1805

Trp Cys Arg Tyr
1810

FIG. 22DD (cont'd)